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OM protein - protein search, using sw model

Run on: June 26, 2005, 15:57:03 ; Search time 43 Seconds
(without alignments)
401.022 Million cell updates/sec

Title: US-10-767-605-2
Perfect score: 1165
Sequence: 1 MFFNRVITLTPSSDVVNS.....DAFKSPRHLPRKRHKICSNS 231

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued Patents AA*
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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1165	100.0	231	US-10-386-972-2	Sequence 2, Appli
2	1160	99.6	231	US-08-721-259-2	Sequence 2, Appli
3	1160	99.6	231	US-09-611-216-2	Sequence 2, Appli
4	423.5	36.4	265	1 US-07-958-551-2	Sequence 2, Appli
5	423.5	36.4	265	1 US-08-129-610-7	Sequence 7, Appli
6	423.5	36.4	265	1 US-08-129-609A-7	Sequence 7, Appli
7	423.5	36.4	265	1 US-08-455-313-7	Sequence 7, Appli
8	423.5	36.4	265	1 US-08-475-924-2	Sequence 2, Appli
9	423.5	36.4	265	1 US-08-657-579A-2	Sequence 2, Appli
10	423.5	36.4	265	3 US-09-224-025-7	Sequence 7, Appli
11	423.5	36.4	265	4 US-09-706-541-7	Sequence 7, Appli
12	423.5	36.4	265	5 PCT-US94-07887-7	Sequence 7, Appli
13	417	35.8	222	1 US-08-129-610-8	Sequence 8, Appli
14	417	35.8	222	1 US-08-129-609A-8	Sequence 8, Appli
15	417	35.8	222	1 US-08-455-313-8	Sequence 8, Appli
16	417	35.8	222	1 US-08-475-924-3	Sequence 3, Appli
17	417	35.8	222	2 US-08-657-579A-3	Sequence 3, Appli
18	417	35.8	222	4 US-09-224-025-8	Sequence 8, Appli
19	417	35.8	222	4 US-09-706-541-8	Sequence 8, Appli
20	417	35.8	222	5 PCT-US94-07887-8	Sequence 8, Appli
21	97	8.3	1833	4 US-08-621-944A-4	Sequence 4, Appli
22	97	8.3	1833	4 US-08-945-567D-4	Sequence 4, Appli
23	97	8.3	1992	4 US-08-621-944A-3	Sequence 3, Appli
24	97	8.3	1992	4 US-08-945-567D-3	Sequence 3, Appli
25	97	8.3	2048	3 US-09-268-347-48	Sequence 48, Appli
26	93	8.0	2123	3 US-08-968-685A-10	Sequence 10, Appli
27	89.5	7.7	624	4 US-09-248-796A-24363	Sequence 24363, A

ALIGNMENTS

RESULT 1

US-10-386-972-2
; Sequence 2, Application US/10386972
; Patent No. 6686452
; GENERAL INFORMATION:
; APPLICANT: Rupar, Mark J.
; APPLICANT: Donovan, William P.
; APPLICANT: Tan, Yuting
; APPLICANT: Slaney, Annette C.
; TITLE OF INVENTION: Bacillus thuringiensis CryET29 Compositions Toxic to Coleopteran
; TITLE OF INVENTION: Insects and Ctenocephalides Spp.
; FILE REFERENCE: MECO-017--2
; CURRENT APPLICATION NUMBER: US/10/386,972
; CURRENT FILING DATE: 2003-03-12
; PRIOR APPLICATION NUMBER: 09/611,216
; PRIOR FILING DATE: 2000-07-06
; PRIOR APPLICATION NUMBER: 08/721,259
; PRIOR FILING DATE: 1996-09-26
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: Patent in version 3.2
; SEQ ID NO 2
; TYPE: PRT
; ORGANISM: Bacillus thuringiensis
US-10-386-972-2

Query Match	100.0%	Score 1165;	DB 4;	Length 231;
Best Local Similarity	100.0%	Pred. No. 2.7e-111;		
Matches 231;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;
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Db	1	MFFNRVITLTPSSDVVNSIIYVAPQYVQALTLAKYFQCAIDGSLRPFDEKALQTA	60	
QY	61	NDIPQAAVNTLNQTVQGGTVQVSVIMDKIVDMKNVLSIVIDNKKFWDQVTAATNTPT	120	
Db	61	NDIPQAAVNTLNQTVQGGTVQVSVIMDKIVDMKNVLSIVIDNKKFWDQVTAATNTPT	120	
QY	121	NLNSQSESAWIFYKEDAHKTSYYNIFALQDEETGGVMATPLPIAFDISVDIEKEKVLV	180	
Db	121	NLNSQSESAWIFYKEDAHKTSYYNIFALQDEETGGVMATPLPIAFDISVDIEKEKVLV	180	
QY	181	VTIKDTENYAVTVKAINVQALQSSRDSKVVDAPFKSPRHLPRKRHKICSNS	231	
Db	181	VTIKDTENYAVTVKAINVQALQSSRDSKVVDAPFKSPRHLPRKRHKICSNS	231	

RESULT 2
US-08-721-259-2
; Sequence 2, Application US/08721259

; Patent No. 6093695
; GENERAL INFORMATION:
; APPLICANT: Rupan, Mark J.
; APPLICANT: Donovan, William P.
; APPLICANT: Tan, Yiping
; APPLICANT: Slaney, Annette C.
; TITLE OF INVENTION: BACILLUS THURINGIENSIS CRYET29
; TITLE OF INVENTION: COMPOSITIONS TOXIC TO COLEOPTERAN
; TITLE OF INVENTION: INSECTS AND CTENOCEPHALIDES spp.
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Arnold, White & Durkee
; CITY: Houston
; STATE: Texas
; COUNTRY: United States of America
; ZIP: 77210
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; FILING DATE: Concurrently Herewith
; APPLICATION NUMBER: US/08/721,259
; CLASSIFICATION: 800
; ATTORNEY/AGENT INFORMATION:
; NAME: Kitchell, Barbara S.
; REGISTRATION NUMBER: 33,928
; REFERENCE/DOCKET NUMBER: MOBT:017
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (512) 418-3000
; TELEFAX: (512) 474-7577
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 231 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-721-259-2

Query Match 99.6%; Score 1160; DB 3; Length 231;
Best Local Similarity 99.6%; Pred. No. 8.6e-111;
Matches 230; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 MFFNRVITLTPSSDVVNYSEIYQVAPQYVNOALTAKYFQGAIDGSLRDFEFKALQIA 60
Db 1 MFFNRVITLTPSSDVVNYSEIYQVAPQYVNOALTAKYFQGAIDGSLRDFEFKALQIA 60
Qy 61 NDIPQAAVNTLNQTVQGVSVMDIKVIDIMKNVLSIVIDNKKFWDQVTAITNTFT 120
Db 61 NDIPQAAVNTLNQTVQGVSVMDIKVIDIMKNVLSIVIDNKKFWDQVTAITNTFT 120
Qy 121 NLNQSSEAWIFYKKEDAKHTSYNNILFAIQDEETGGVMATLPIAFDISVDIEKEKVL 180
Db 121 NLNQSSEAWIFYKKEDAKHTSYNNILFAIQDEETGGVMATLPIAFDISVDIEKEKVL 180
Qy 181 VTIKDTENYAVTVKAINVQALQSSRDSKVVDFAFKSPRHLPRKRHKICSNS 231
Db 181 VTIKDTENYAVTVKAINVQALQSSRDSKVVDFAFKSPRHLPRKRHKICSNS 231

RESULT 3
US-09-611-216-2
; Sequence 2, Application US/09611216
; Patent No. 6537756
; GENERAL INFORMATION:
; APPLICANT: Rupan, Mark J.
; APPLICANT: Donovan, William P.
; APPLICANT: Tan, Yiping
; APPLICANT: Slaney, Annette C.
; TITLE OF INVENTION: BACILLUS THURINGIENSIS CRYET29
; TITLE OF INVENTION: COMPOSITIONS TOXIC TO COLEOPTERAN

; TITLE OF INVENTION: INSECTS AND CTENOCEPHALIDES spp.
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Arnold, White & Durkee
; CITY: Houston
; STATE: Texas
; COUNTRY: United States of America
; ZIP: 77210
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; FILING DATE: US/09/611,216
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/721,259
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Kitchell, Barbara S.
; REGISTRATION NUMBER: 33,928
; REFERENCE/DOCKET NUMBER: MOBT:017
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (512) 418-3000
; TELEFAX: (512) 474-7577
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 231 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-09-611-216-2

Query Match 99.6%; Score 1160; DB 4; Length 231;
Best Local Similarity 99.6%; Pred. No. 8.6e-111;
Matches 230; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 MFFNRVITLTPSSDVVNYSEIYQVAPQYVNOALTAKYFQGAIDGSLRDFEFKALQIA 60
Db 1 MFFNRVITLTPSSDVVNYSEIYQVAPQYVNOALTAKYFQGAIDGSLRDFEFKALQIA 60
Qy 61 NDIPQAAVNTLNQTVQGVSVMDIKVIDIMKNVLSIVIDNKKFWDQVTAITNTFT 120
Db 61 NDIPQAAVNTLNQTVQGVSVMDIKVIDIMKNVLSIVIDNKKFWDQVTAITNTFT 120
Qy 121 NLNQSSEAWIFYKKEDAKHTSYNNILFAIQDEETGGVMATLPIAFDISVDIEKEKVL 180
Db 121 NLNQSSEAWIFYKKEDAKHTSYNNILFAIQDEETGGVMATLPIAFDISVDIEKEKVL 180
Qy 181 VTIKDTENYAVTVKAINVQALQSSRDSKVVDFAFKSPRHLPRKRHKICSNS 231
Db 181 VTIKDTENYAVTVKAINVQALQSSRDSKVVDFAFKSPRHLPRKRHKICSNS 231

RESULT 4
US-07-958-551-2
; Sequence 2, Application US/07958551
; Patent No. 5302387
; GENERAL INFORMATION:
; APPLICANT: Payne, Jewel M.
; APPLICANT: Kennedy, Keith M.
; APPLICANT: Randall, John Brookes
; APPLICANT: Brower, David Orlin
; TITLE OF INVENTION: Bacillus thuringiensis Isolates Active Against
; TITLE OF INVENTION: Cockroaches and Genes Encoding Cockroach-Active
; TITLE OF INVENTION: Toxins
; NUMBER OF SEQUENCES: 2
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: David R. Saliwanchik
; STREET: 2421 N.W. 41st Street, Suite A-1

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; CITY: Gainesville
; STATE: FL
; COUNTRY: USA
; ZIP: 32606
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/958,551
; FILING DATE: October 19, 1992
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/788,654
; FILING DATE: No. 5302387ember 6, 1991
; NAME:
; ATTORNEY/AGENT INFORMATION:
; NAME: Saliwanchik, David R.
; REGISTRATION NUMBER: 31,794
; REFERENCE/DOCKET NUMBER: M/J 101.C2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 904-375-8100
; TELEFAX: 904-372-5800
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 265 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; HYPOTHETICAL: YES
; ANTI-SENSE: NO
; ORIGINAL SOURCE:
; ORGANISM: Bacillus thuringiensis
; STRAIN: neoleonensis
; INDIVIDUAL ISOLATE: PS201T6
; IMMEDIATE SOURCE:
; LIBRARY: LambdaGem (TM)-11 Library of Kenneth E. Narva
; CLONE: 201T635
; US-07-958-551-2

Query Match 36.4%; Score 423.5; DB 1; Length 265;
Best Local Similarity 40.9%; Pred. No. 3e-35;
Matches 94; Conservative 47; Mismatches 72; Indels 17; Gaps 6;

Qy 5 RVITLTPSSDVVNYSEIYQVA----POYVNOALTAKYFOGAI-----DGSTLRPDPFE 54
Db 38 RVYILKV--KDPIDTTQLLEITEIENPNVYVLAQIAAFAFDALVPTETFEGEAIRFSMP 95
Qy 55 KALQIANDI-POAAVNTLNQTVQGVSVIMDKIVDMKNVLSIVIDNKKFWDQVTA 113
Db 96 KGLEVAKTIQPGAVVAYTDQTLSSNNQVSVIMDRVSVLKVTVMGVALSG-SIITQLTA 154
Qy 114 AITNTFTNLNQSBSAWIPYKEDAHKTSYYNIFAIQDEETGGMATLPIAFDISVDI 173
Db 155 AITDTFTNLTKDSAWVFWGKETSQNTYNNVNFALQNETTGRVVMCVPIGPBIRVET 214
Qy 174 EKEKVLFTVIKDTENYATVAVVAVVQALQSRDSKVDV---AFKSPRHL 220
Db 215 DKRTVLFTTKDYANYSVNIQTLRPAQLIDSRALSINDLSEALRSSKYL 264

US-08-129-610-7

RESULT 5
US-08-129-610-7
; Sequence 7, Application US/08129610
; Patent No. 5436002
; GENERAL INFORMATION:
; APPLICANT: Jewel Payne
; APPLICANT: Kenneth Narva
; APPLICANT: Kendrick Akira Uyeda
; APPLICANT: Christine Julie Stalder
; APPLICANT: Tracy Ellis Michaels

; TITLE OF INVENTION: No. 5436002el Bacillus thuringiensis Isolates and Toxins
; NUMBER OF SEQUENCES: 10
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: David R. Saliwanchik
; STREET: 2421 N.W. 41st Street, Suite A-1
; CITY: Gainesville
; STATE: FL
; COUNTRY: USA
; ZIP: 32606
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/129,610
; FILING DATE:
; CLASSIFICATION: 800
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/093,199
; FILING DATE: 15-JUL-1993
; NAME:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/977,350
; FILING DATE: 17-NOV-1992
; NAME:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/746,751
; FILING DATE: 21-AUG-1991
; NAME:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/708,266
; FILING DATE: 28-MAY-1991
; NAME:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/647,399
; FILING DATE: 29-JAN-1991
; NAME:
; ATTORNEY/AGENT INFORMATION:
; NAME: Saliwanchik, David R.
; REGISTRATION NUMBER: 31,794
; REFERENCE/DOCKET NUMBER: MA55CCD.C1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 904-375-8100
; TELEFAX: 904-372-5800
; INFORMATION FOR SEQ ID NO: 7:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 265 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; HYPOTHETICAL: YES
; ANTI-SENSE: NO
; ORIGINAL SOURCE:
; ORGANISM: Bacillus thuringiensis
; STRAIN: neoleonensis
; INDIVIDUAL ISOLATE: PS201T6
; IMMEDIATE SOURCE:
; LIBRARY: LambdaGem (TM)-11 Library of Kenneth E. Narva
; CLONE: 201T635
; US-08-129-610-7

Query Match 36.4%; Score 423.5; DB 1; Length 265;
Best Local Similarity 40.9%; Pred. No. 3e-35;
Matches 94; Conservative 47; Mismatches 72; Indels 17; Gaps 6;

Qy 5 RVITLTPSSDVVNYSEIYQVA----POYVNOALTAKYFOGAI-----DGSTLRPDPFE 54
Db 38 RVYILKV--KDPIDTTQLLEITEIENPNVYVLAQIAAFAFDALVPTETFEGEAIRFSMP 95
Qy 55 KALQIANDI-POAAVNTLNQTVQGVSVIMDKIVDMKNVLSIVIDNKKFWDQVTA 113
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Db 96 KGLEVAKTIQPKGAVVAYTDQTLQSNNQVSMIDRVISVLKTMGVVALSG-SIITQLTA 154
Qy 114 AITNFTNLNSQSEAWIFYKEDAHKTSYYNILFAIQDBETGGMATLPIAFDISVDI 173
Db 155 AITDFTNLNTQKDSAWFMWKGKTSHTQNTYTNVMFAIQNETTGRVMMCVPIGPEIRVFT 214
Qy 174 EKEKVLFTIKDTENYAVTVKAINVVQALQSSRDSKVD---AFKSPRHL 220
Db 215 DKRTVLFTTKDYANYSVNIQTLRPAQPLIDSRALSINDLSEALRSSKYL 264

RESULT 6
US-08-129-609A-7
; Sequence 7, Application US/08129609A
; Patent No. 5489432
; GENERAL INFORMATION:
; APPLICANT: Jewel Payne
; APPLICANT: M. Keith Kennedy
; APPLICANT: John Brookes Randall
; APPLICANT: David Orlin Brower
; APPLICANT: H. Ernest Schnepf
; TITLE OF INVENTION: Bacillus thuringiensis Isolates Active
; AGAINST COCKROACHES AND GENES ENCODING COCKROACH-ACTIVE TOXINS
; NUMBER OF SEQUENCES: 10
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: David R. Saliwanchik
; STREET: 2421 N.W. 41st Street, Suite A-1
; CITY: Gainesville
; STATE: FL
; COUNTRY: USA
; ZIP: 32606
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/129,609A
; FILING DATE: 30-SEP-1993
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/958,551
; FILING DATE: 19-OCT-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/788,654
; FILING DATE: 6-NOV-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Saliwanchik, David R.
; REGISTRATION NUMBER: 31,794
; REFERENCE/DOCKET NUMBER: M/J 101.C2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 904-375-8100
; TELEFAX: 904-372-5800
; INFORMATION FOR SEQ ID NO: 7:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 265 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; HYPOTHETICAL: YES
; ANTI-SENSE: NO
; ORIGINAL SOURCE:
; ORGANISM: Bacillus thuringiensis
; STRAIN: neoleoensis
; INDIVIDUAL ISOLATE: PS201T6
; IMMEDIATE SOURCE:
; LIBRARY: LambdaGem (TM)-11 Library of Kenneth E. Narva
; CLONE: 201T635
US-08-129-609A-7
Query Match 36.4%; Score 423.5; DB 1; Length 265;
Best Local Similarity 40.9%; Pred. No. 3e-35;
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Matches 94; Conservative 47; Mismatches 72; Indels 17; Gaps 6;
Qy 5 RVILTPSSDVNYSIYQVA---PQYVNOALTAKYFQGA-----DGSTLRPDE 54
Db 38 RVIIYLVK--KDPIDTTLQLEITEIENPNYVLQALAAAFQDALVPTTEFEGEAIRFSMP 95
Qy 55 KALQIANDI--PQAAVAVNTNQVQGTQVQSVMDIKVIDIMKNVLSIVIDNKKFWDQVTA 113
Db 96 KGLEVAKTIQPKGAVVAYTDQTLQSNNQVSMIDRVISVLKTMGVVALSG-SIITQLTA 154
Qy 114 AITNFTNLNSQSEAWIFYKEDAHKTSYYNILFAIQDBETGGMATLPIAFDISVDI 173
Db 155 AITDFTNLNTQKDSAWFMWKGKTSHTQNTYTNVMFAIQNETTGRVMMCVPIGPEIRVFT 214
Qy 174 EKEKVLFTIKDTENYAVTVKAINVVQALQSSRDSKVD---AFKSPRHL 220
Db 215 DKRTVLFTTKDYANYSVNIQTLRPAQPLIDSRALSINDLSEALRSSKYL 264

RESULT 7
US-08-455-313-7
; Sequence 7, Application US/08455313
; Patent No. 5635480
; GENERAL INFORMATION:
; APPLICANT: Jewel Payne
; APPLICANT: Kenneth Narva
; APPLICANT: Kendrick Akira Uyeda
; APPLICANT: Christine Julie Stalder
; APPLICANT: Tracy Ellis Michaels
; TITLE OF INVENTION: NO. 5635480el Bacillus thuringiensis Isolates and Toxins
; NUMBER OF SEQUENCES: 10
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: David R. Saliwanchik
; STREET: 2421 N.W. 41st Street, Suite A-1
; CITY: Gainesville
; STATE: FL
; COUNTRY: USA
; ZIP: 32606
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/455,313
; FILING DATE: 31-MAY-1995
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/129,610
; FILING DATE: 30-SEP-1993
; APPLICATION NUMBER: US 08/093,199
; FILING DATE: 15-JUL-1993
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/977,350
; FILING DATE: 17-NOV-1992
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/746,751
; FILING DATE: 21-AUG-1991
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/708,266
; FILING DATE: 28-MAY-1991
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/647,399
; FILING DATE: 29-JAN-1991
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: Saliwanchik, David R.
; REGISTRATION NUMBER: 31,794
; REFERENCE/DOCKET NUMBER: MA55CCD.C1
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; REGISTRATION NUMBER: 39,355
; REFERENCE/DOCKET NUMBER: MA96.C1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 352-375-8100
; TELEFAX: 352-372-5800
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 265 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; HYPOTHETICAL: YES
; ANTI-SENSE: NO
; ORIGINAL SOURCE:
; ORGANISM: Bacillus thuringiensis
; STRAIN: neolecensis
; INDIVIDUAL ISOLATE: PS201T6
; IMMEDIATE SOURCE:
; LIBRARY: LambdaGem (TM)-11 Library of Kenneth E. Narva
; CLONE: 201T635
; US-08-657-579A-2

Query Match 36.4%; Score 423.5; DB 2; Length 265;
Best Local Similarity 40.9%; Pred. No. 3e-35;
Matches 94; Conservative 47; Mismatches 72; Indels 17; Gaps 6;

QY 5 RVITLTPSSDVVNYSEIYQVA---POYVNAQLTLAKYFQGA1-----DGSTLRFPDFE 54
DB 38 RVYLVKV--KDPIDTTLLEITEIENPNYVLQALAAAFQDALVPTETETGEAIRFSMP 95

QY 55 KALQIANDI-POAAVNTLNQTVQGVTVQVSMVDKIVDMKNVLSIVIDNKKFWQVTA 113
DB 96 KGLEVAKTIOPKGAVVAYTDQTLSSNNQVSMIDRVISVLKTMGVVALSG-SIITQLTA 154

QY 114 AITNTFTNLNSESSEAWIFYYKEDAHKTSYYNILFAIQDEBTGVMTLP1AFDISYDI 173
DB 155 AITDTFTNLNQTQKDSAWVFWGKETSHTQNTYTNVWFALQNETTGRVMMCVPIGFEIRVFT 214

QY 174 EKEKLVFTTIKDTENYAVTVKAINVVQALQSSRSKVVDD---APKSPRHL 220
DB 215 DKRTVLFTTKDYANYSVNIQTLRPAQPLIDSRALSINDLSEALRSSKYL 264

RESULT 10
US-09-224-025-7
; Sequence 7, Application US/09224025
; Patent No. 6150165
; GENERAL INFORMATION:
; APPLICANT: Jewel Payne
; APPLICANT: Kenneth Narva
; APPLICANT: Kendrick Akira Uyeda
; APPLICANT: Christine Julie Stalder
; APPLICANT: Tracy Ellis Michaels
; TITLE OF INVENTION: No. 6150165el Bacillus thuringiensis Isolates and Toxins
; NUMBER OF SEQUENCES: 10
; CORRESPONDENCE ADDRESS:
; ADDRESS: David R. Saliwanchik
; STREET: 2421 N.W. 41st Street, Suite A-1
; CITY: Gainesville
; STATE: FL
; COUNTRY: USA
; ZIP: 32606
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/224,025
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:

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; APPLICATION NUMBER: 08/455,313
; FILING DATE: 08/093,199
; APPLICATION NUMBER: US 08/093,199
; FILING DATE: 15-JUL-1993
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/977,350
; FILING DATE: 17-NOV-1992
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/746,751
; FILING DATE: 21-AUG-1991
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/708,266
; FILING DATE: 28-MAY-1991
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/647,399
; FILING DATE: 29-JAN-1991
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Saliwanchik, David R.
; REGISTRATION NUMBER: 31,794
; REFERENCE/DOCKET NUMBER: MA55CCD.C1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 904-375-8100
; TELEFAX: 904-372-5800
; INFORMATION FOR SEQ ID NO: 7:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 265 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; HYPOTHETICAL: YES
; ANTI-SENSE: NO
; ORIGINAL SOURCE:
; ORGANISM: Bacillus thuringiensis
; STRAIN: neolecensis
; INDIVIDUAL ISOLATE: PS201T6
; IMMEDIATE SOURCE:
; LIBRARY: LambdaGem (TM)-11 Library of Kenneth E. Narva
; CLONE: 201T635
; US-09-224-025-7

Query Match 36.4%; Score 423.5; DB 3; Length 265;
Best Local Similarity 40.9%; Pred. No. 3e-35;
Matches 94; Conservative 47; Mismatches 72; Indels 17; Gaps 6;

QY 5 RVITLTPSSDVVNYSEIYQVA---POYVNAQLTLAKYFQGA1-----DGSTLRFPDFE 54
DB 38 RVYLVKV--KDPIDTTLLEITEIENPNYVLQALAAAFQDALVPTETETGEAIRFSMP 95

QY 55 KALQIANDI-POAAVNTLNQTVQGVTVQVSMVDKIVDMKNVLSIVIDNKKFWQVTA 113
DB 96 KGLEVAKTIOPKGAVVAYTDQTLSSNNQVSMIDRVISVLKTMGVVALSG-SIITQLTA 154

QY 114 AITNTFTNLNSESSEAWIFYYKEDAHKTSYYNILFAIQDEBTGVMTLP1AFDISYDI 173
DB 155 AITDTFTNLNQTQKDSAWVFWGKETSHTQNTYTNVWFALQNETTGRVMMCVPIGFEIRVFT 214

QY 174 EKEKLVFTTIKDTENYAVTVKAINVVQALQSSRSKVVDD---APKSPRHL 220
DB 215 DKRTVLFTTKDYANYSVNIQTLRPAQPLIDSRALSINDLSEALRSSKYL 264

RESULT 11
US-09-706-541-7
; Sequence 7, Application US/09706541
; Patent No. 6689743
; GENERAL INFORMATION:
; APPLICANT: Jewel Payne

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; ; SEQUENCE CHARACTERISTICS:
; LENGTH: 265 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; HYPOTHETICAL: YES
; ANTI-SENSE: NO
; ORIGINAL SOURCE:
; ORGANISM: Bacillus thuringiensis
; STRAIN: neoleoensis
; INDIVIDUAL ISOLATE: PS201T6
; IMMEDIATE SOURCE:
; LIBRARY: LambdaGem (TM)-11 Library of Kenneth E. Narva
; CLONE: 201T635
PCT-US94-07887-7

Query Match 36.4%; Score 423.5; DB 5; Length 265;
Best Local Similarity 40.9%; Pred. No. 3e-35; Indels 17; Gaps 6;
Matches 94; Conservative 47; Mismatches 72; Indels 17; Gaps 6;

Qy 5 RVILTPSSDVNNSEIYQVA----POYVNOALTAKYFGAI-----DGSTLRFDFE 54
Db 38 RVILKV--KPIDTQLLEITEIENPNYVLQALAAAFQDALVPTETEFGEAIRFSMP 95
Qy 55 KALQIANDI-POAAVNTLNQTVQSGTVQVSMIDKIVDIMKNVLSIVIDNKKFWDQVTA 113
Db 96 KGLEVAKTIQPKGAVVAYTDTQLSQSNQVSMIDRVISVLKTVNGVALSG-SIITQLTA 154
Qy 114 AITNFTNLNQSSEAWIFYKKEDAHTKTSYYNINLFAIQDEETGGVMATLPFAFDISVDI 173
Db 155 AITDFTNLNQTQKSAWVFWGKETSHTQNTYNNVWFALQNETTGRVMMCVPIGEIRVFT 214
Qy 174 EKEKLVFTIKDENTYAVTVKAINVVQALQSSRDSKVVD---AFKSPRHL 220
Db 215 DKRTVLFTTKDYANSVNIQTLRFAQLIDSRALSINDLSEALRSSKYL 264

RESULT 13
US-08-129-610-8
; Sequence 8, Application US/08129610
; Patent No. 5436002
; GENERAL INFORMATION:
; APPLICANT: Jewel Payne
; APPLICANT: Kenneth Narva
; APPLICANT: Kendrick Akira Uyeda
; APPLICANT: Christine Julie Stalder
; APPLICANT: Tracy Ellis Michaels
; TITLE OF INVENTION: No. 5436002el Bacillus thuringiensis Isolates and Toxins
; NUMBER OF SEQUENCES: 10
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: David R. Saliwanchik
; STREET: 2421 N.W. 41st Street, Suite A-1
; CITY: Gainesville
; STATE: FL USA
; COUNTRY: USA
; ZIP: 32606
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/129,610
; FILING DATE:
; CLASSIFICATION: 800
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/093,199
; FILING DATE: 15-JUL-1993
; NAME:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/977,350
; FILING DATE: 17-NOV-1992
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; ; NAME:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/746,751
; FILING DATE: 21-AUG-1991
; NAME:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/708,266
; FILING DATE: 28-MAY-1991
; NAME:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/647,399
; FILING DATE: 29-JAN-1991
; NAME:
; ATTORNEY/AGENT INFORMATION:
; NAME: Saliwanchik, David R.
; REGISTRATION NUMBER: 31,794
; REFERENCE/DOCKET NUMBER: MA55CCD.C1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 904-375-8100
; TELEFAX: 904-372-5800
; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 222 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; HYPOTHETICAL: YES
; ANTI-SENSE: NO
; ORIGINAL SOURCE:
; ORGANISM: Bacillus thuringiensis
; STRAIN: neoleoensis
; INDIVIDUAL ISOLATE: PS201T6
US-08-129-610-8

Query Match 35.8%; Score 417; DB 1; Length 222;
Best Local Similarity 41.9%; Pred. No. 1.1e-34;
Matches 91; Conservative 42; Mismatches 72; Indels 12; Gaps 5;

Qy 15 DVNYSIYQVA-POYVNOALTAKYFGAI-----DGSTLRFDFEALQIANDI-POA 66
Db 6 DTTQLLEITEIENPNYVLQALAAAFQDALVPTETEFGEAIRFSMPKGLEVAKTIQPKG 65
Qy 67 AVVNTLNQTVQSGTVQVSMIDKIVDIMKNVLSIVIDNKKFWDQVTAITNFTNLN 126
Db 66 AVAYTDQLSQSNQVSMIDRVISVLKTVNGVALSG-SIITQTAITDFTNLN 124
Qy 127 SEAWIFYKKEDAHTKTSYYNINLFAIQDEETGGVMATLPFAFDISVDIEKEKLVFTIKDT 186
Db 125 DSAVFWGKETSHQNTYNNVWFALQNETTGRVMMCVPIGEIRVFTDKRTVLPLTTKDY 184
Qy 187 ENYAVTVKAINVVQALQSSRDSKVVD---AFKSPRHL 220
Db 185 ANYSVNIQTLRFAQLIDSRALSINDLSEALRSSKYL 221

RESULT 14
US-08-129-609A-8
; Sequence 8, Application US/08129609A
; Patent No. 5489432
; GENERAL INFORMATION:
; APPLICANT: Jewel Payne
; APPLICANT: M. Keith Kennedy
; APPLICANT: John Brookes Randall
; APPLICANT: David Orlin Brower
; APPLICANT: H. Ernest Schnepf
; TITLE OF INVENTION: Bacillus thuringiensis Isolates Active
; TITLE OF INVENTION: Against Cockroaches and Genes Encoding Cockroach-Active Toxins
; NUMBER OF SEQUENCES: 10
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: David R. Saliwanchik
; STREET: 2421 N.W. 41st Street, Suite A-1
; CITY: Gainesville
```


STATE: FL
COUNTRY: USA
ZIP: 32606
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/129,609A
FILING DATE: 30-SEP-1993
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/958,551
FILING DATE: 19-OCT-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/788,654
FILING DATE: 6-NOV-1991
ATTORNEY/AGENT INFORMATION:
NAME: Saliwanchik, David R.
REGISTRATION NUMBER: 31,794
REFERENCE/DOCKET NUMBER: M/J 101.C2
TELECOMMUNICATION INFORMATION:
TELEPHONE: 904-375-8100
TELEFAX: 904-372-5800

INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 222 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHETICAL: YES
ANTI-SENSE: NO
ORIGINAL SOURCE:
ORGANISM: Bacillus thuringiensis
STRAIN: neoleoensis
INDIVIDUAL ISOLATE: PS201T6
US-08-129-609A-8

Query Match 35.8%; Score 417; DB 1; Length 222;
Best Local Similarity 41.9%; Pred. No. 1.1e-34;
Matches 91; Conservative 42; Mismatches 72; Indels 12; Gaps 5;
QY 15 DVVNYSEIYQVA-POYVNAQALTAKYFQGA-----DGSTLRFDFEKALQIANDI-PQA 66
DB 6 DTTQLLEITEIENPNVYLQALQALAAAFQDALVPTETFEGEAIRFSMPKGLVAKTIQPKG 65
QY 67 AVVNTLNQTVQGGTVQVSMIDKIVDMKNVLSIVIDNKKFWDQVTAITNTFTNLNSQE 126
DB 66 AVVAYTDQTLQSNNQVSMIDRVISVLKTVMGVALSG-SIITQLTAITDTFTNLNTQK 124
QY 127 SEAWIFYYKEDAHKTSYYNIFALQDEBTGGMATLPIAFDISVDIEKEKLVFTIKDT 186
DB 125 DSAAVFWGKETSQHTNYTNVWFALQNETTGRVMMCMVPGFEIRVFTDKRTFLFTTKDY 184
QY 187 ENYAVTVKAINVQALQSRDSKVVD---AFKSPRHL 220
DB 185 ANYSVNIQTLRPAQPLIDSRALSINDLSEALRSSKYL 221

RESULT 15
US-08-455-313-8
Sequence 8, Application US/08455313
Patent No. 5635480
GENERAL INFORMATION:
APPLICANT: Jewel Payne
APPLICANT: Kenneth Narva
APPLICANT: Kendrick Akira Uyeda
APPLICANT: Christine Julie Stalder
APPLICANT: Tracy Ellis Michaels
TITLE OF INVENTION: No. 5635480el Bacillus thuringiensis Isolates and Toxins
NUMBER OF SEQUENCES: 10

CORRESPONDENCE ADDRESS:
ADDRESSEE: David R. Saliwanchik
STREET: 2421 N.W. 41st Street, Suite A-1
CITY: Gainesville
STATE: FL
COUNTRY: USA
ZIP: 32606
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/455,313
FILING DATE: 31-MAY-1995
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/129,610
FILING DATE: 30-SEP-1993
APPLICATION NUMBER: US 08/093,199
FILING DATE: 15-JUL-1993
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/977,350
FILING DATE: 17-NOV-1992
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/746,751
FILING DATE: 21-AUG-1991
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/708,266
FILING DATE: 28-MAY-1991
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/647,399
FILING DATE: 29-JAN-1991
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: Saliwanchik, David R.
REGISTRATION NUMBER: 31,794
REFERENCE/DOCKET NUMBER: MA55CCD.C1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 904-375-8100
TELEFAX: 904-372-5800

INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 222 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHETICAL: YES
ANTI-SENSE: NO
ORIGINAL SOURCE:
ORGANISM: Bacillus thuringiensis
STRAIN: neoleoensis
INDIVIDUAL ISOLATE: PS201T6
US-08-455-313-8

Query Match 35.8%; Score 417; DB 1; Length 222;
Best Local Similarity 41.9%; Pred. No. 1.1e-34;
Matches 91; Conservative 42; Mismatches 72; Indels 12; Gaps 5;

QY 15 DVVNYSEIYQVA-POYVNAQALTAKYFQGA-----DGSTLRFDFEKALQIANDI-PQA 66
DB 6 DTTQLLEITEIENPNVYLQALQALAAAFQDALVPTETFEGEAIRFSMPKGLVAKTIQPKG 65
QY 67 AVVNTLNQTVQGGTVQVSMIDKIVDMKNVLSIVIDNKKFWDQVTAITNTFTNLNSQE 126
DB 66 AVVAYTDQTLQSNNQVSMIDRVISVLKTVMGVALSG-SIITQLTAITDTFTNLNTQK 124
QY 127 SEAWIFYYKEDAHKTSYYNIFALQDEBTGGMATLPIAFDISVDIEKEKLVFTIKDT 186

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: June 26, 2005, 15:47:47 ; Search time 174 Seconds
(without alignments)
679.829 Million cell updates/sec

Title: US-10-767-605-2

Perfect score: 1165
Sequence: 1 MFNRVTLTVPSDDVNNYS.....DAFKSPRHLPRKRHKICSNS 231

Scoring table:
BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 45 summaries

Database : UniProt_03.*

1: uniprot_sprot.*
2: uniprot_trembl.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

* Result No.	Score	Query Match	Length	ID	Description
1	1160	99.6	231	2 Q93M48	Q93M48 bacillus th
2	637	54.7	259	1 CYAA_BACTY	Q04470 bacillus th
3	637	54.7	259	2 Q71KW8	Q71KW8 bacillus th
4	597	51.2	260	2 Q8VNX0	Q8VNX0 bacillus th
5	595	51.1	263	1 CYBA_BACTI	Q45723 bacillus th
6	592.5	50.9	263	1 CYBB_BACTJ	Q32322 bacillus th
7	586	50.3	263	2 Q9L878	Q9L878 bacillus th
8	456	39.1	249	1 CXAA_BACTI	P05069 bacillus th
9	448	38.5	157	2 O52298	O52298 bacillus th
10	448	38.5	157	2 Q7BVD4	Q7BVD4 bacillus th
11	444	38.1	156	2 Q30895	Q30895 bacillus th
12	443	38.0	156	2 Q9R9C0	Q9R9C0 bacillus th
13	442	37.9	156	2 Q30969	Q30969 bacillus th
14	423.5	36.4	265	1 CXBA_BACTW	Q45790 bacillus th
15	416.5	35.8	250	1 CXAB_BACTV	P94594 bacillus th
16	344.5	29.6	525	2 Q8KNJ9	Q8KNJ9 bacillus th
17	151.5	13.0	217	2 Q6USC4	Q6USC4 volvariella
18	105.5	9.1	880	2 Q91R5	Q91R5 clostridium
19	105.5	9.1	1830	2 Q7YV0	Q7YV0 cryptospori
20	105.5	9.1	2528	2 Q86J36	Q86J36 dictyosteli
21	103	8.8	477	2 Q68960	Q68960 helicobacte
22	103	8.8	477	2 Q25326	Q25326 helicobacte
23	102.5	8.8	981	2 Q8MET8	Q8MET8 parachlanyd
24	101	8.7	477	2 Q9ZLM7	Q9ZLM7 helicobacte
25	99.5	8.5	4540	1 YDHC_PARTF	Q27171 paramecium
26	98.5	8.5	201	1 Y007_NPVAC	P24650 autographa
27	97.5	8.4	1442	2 Q83858	Q83858 nilaparvata
28	97	8.3	565	2 Q6CT48	Q6CT48 kluyveromyc
29	96.5	8.3	343	1 HRCA_BACSU	P54999 bacillus su
30	95.5	8.2	421	1 TYPH_MYCGE	P47297 mycoplasma
31	95.5	8.2	1876	2 Q8DQNS	Q8DQNS streptococc

32 95 8.2 1076 1 CARB_BUCEP PS9448 buchnera ap
33 94.5 8.1 249 2 Q9K9Y9 Q9K9Y9 bacillus ha
34 94.5 8.1 393 1 RPN9_YEAST Q04062 saccharomyc
35 94 8.1 498 2 Q7QSH6 Q7QSH6 giardia lam
36 93.5 8.0 660 2 Q81EH1 Q81EH1 bacillus ce
37 93 8.0 773 2 Q8KZM6 Q8KZM6 piscophilus
38 92.5 7.9 1018 2 Q8RFH6 Q8RFH6 fusobacteri
39 92.5 7.9 4688 2 Q9PQ08 Q9PQ08 ureaplasma
40 92 7.9 297 2 Q7RGC0 Q7RGC0 plasmodium
41 92 7.9 297 2 Q7NBJ7 Q7NBJ7 mycoplasma
42 92 7.9 678 2 Q8XIX7 Q8XIX7 clostridium
43 92 7.9 845 2 Q7R8M2 Q7R8M2 plasmodium
44 92 7.9 1147 2 Q6LEZ7 Q6LEZ7 plasmodium
45 92 7.9 4780 2 Q8IE54 Q8IE54 plasmodium

ALIGNMENTS

RESULT 1

Q93M48 ID Q93M48 PRELIMINARY; PRT; 231 AA.
AC Q93M48; 01-DEC-2001 (Tremblrel. 19, Created)
DT 01-DEC-2001 (Tremblrel. 19, Last sequence update)
DE 01-OCT-2003 (Tremblrel. 25, Last annotation update)
DS Insecticidal crystal protein CryET29.
OS Bacillus thuringiensis.
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
OX NCBI_TaxID=1428;
RN [1]
RP SEQUENCE FROM N.A.
RA Rupar M.J., Donovan W.F., Tan Y., Slaney A.C.;
RL Submitted (MAY-2001) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RA Baum J.A.;
RL Submitted (APR-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY030096; AAK50455.1; -.
DR HSSP; Q04470; 1CBY.
DR GO; GO:0005576; C:extracellular; IEA.
DR GO; GO:0009405; P:pathogenesis; IEA.
DR GO; GO:0042243; P:spore wall assembly (sensu Bacteria); IEA.
DR InterPro; IPR001615; Endotoxin_CytB.
DR Pfam; PF01338; Bac thur toxin; 1.
DR ProDom; PD009844; Endotoxin_CytB; 1.
SQ SEQUENCE 231 AA; 26194 MW; D3734D9E31E44313 CRC64;

Query Match 99.6%; Score 1160; DB 2; Length 231;

Best Local Similarity 99.6%; Pred. No. 7.1e-80;

Matches 230; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 MFNRVTLTVPSDDVNNYSIYQVAPQYNQALTLAKYFOGADGSLRDFEKAQIA 60
Db 1 MFNRVTLTVPSDDVNNYSIYQVAPQYNQALTLAKYFOGADGSLRDFEKAQIA 60
Qy 61 NDIPQAAVNTLNTQVQGVQVSWMDIKVIDIMKNVLSIVIDNKKFWDQVTAITNTFT 120
Db 61 NDIPQAAVNTLNTQVQGVQVSWMDIKVIDIMKNVLSIVIDNKKFWDQVTAITNTFT 120
Qy 121 NLNQSSEAMIFYKKDAHKTSYYNYILFAIQDEETGGVMATLPIAFDISVDIEKEKVL 180
Db 121 NLNQSSEAMIFYKKDAHKTSYYNYILFAIQDEETGGVMATLPIAFDISVDIEKEKVL 180
Qy 181 VTIKDTENYAVTVKAIINNVQALQSSRSKVVDAKSPRHLPRKRHKICSNS 231
Db 181 VTIKDTENYAVTVKAIINNVQALQSSRSKVVDAKSPRHLPRKRHKICSNS 231

RESULT 2

CYAA_BACTY ID CYAA_BACTY STANDARD; PRT; 259 AA.
AC Q04470;


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CC -!- DEVELOPMENTAL STAGE: The crystal protein is produced during
CC sporulation and is accumulated both as an inclusion and as part of
CC the spore coat.
CC -!- FM: Active after proteolytic processing (By similarity).
CC -!- SIMILARITY: Belongs to the cytI/cyt2 endotoxin family.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; U82519; AAB93477.1; -.
DR HSSP; Q04470; 1CBY.
DR InterPro; IPR001615; Endotoxin CytB.
DR Pfam; PF01338; Bac thur toxin; 1.
DR ProDom; PD009844; Endotoxin CytB; 1.
KW Direct protein sequencing; Sporulation; Toxin.
SQ SEQUENCE 263 AA; 30059 MW; BDB7B72CDE090D9D CRC64;

Query Match 50.9%; Score 592.5; DB 1; Length 263;
Best Local Similarity 55.2%; Pred. No. 6.7e-37;
Matches 116; Conservative 40; Mismatches 53; Indels 1; Gaps 1;

QY 5 RVILTVPSDDVNVYSEIYQVAPQVYVQALTLAKYFQGAIDGSTLRPFKALQIANDIP 64
DB 30 RHIALTVPSDDITNFNEIFVEYPOYIAQIRLTNTFQGAIDPLTLNPFKALQIANGLP 89
QY 65 QAAVNTLNQTVQCGTVQVSVMDIKVIDIMKNVLSIVIDNKKFWDQVTAATNTFTNLS 124
DB 90 NAGVTGIIQSVIHQTEVSVWISQIKETIIRSVGLVINSANFNWVSVVSAITNTFTNLEP 149
QY 125 QESBAWIFYKEDAHKTSYYNIIIPAIQDEETGGVMATLPFAFISVDIEKEKVLFTVIK 184
DB 150 QVDENWIVRNLSATQTSFYKILFSIQNEDTGRFMAILPIAFETVDVQKQLLFITIR 206
QY 185 DTENYAVTVKAINVVQALQSSRDSKVVDAPKSPRH-LPRKHKICSN 230
DB 210 DSARYEVKMKALTIVVQALL-DSYNAPIIDVFNVRNYSILHRPNHNLQN 255

RESULT 8
CXAA_BACTI STANDARD; PRT; 249 AA.
ID_CXAA_BACTI
AC P05069; P05628;
DT 13-AUG-1987 (Rel. 05, Created)
DT 13-AUG-1987 (Rel. 05, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Type-1Aa cytolytic delta-endotoxin (27 kDa cytolytic toxin).
GN Name=cyt1Aa; Synonyms=cytA;
OS Bacillus thuringiensis (subsp. israelensis), and
OC Bacillus thuringiensis (subsp. morrisoni).
OG Plasmid 72 Kb.
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
OX NCBI_TaxID=1430, 1441;
RN [1]
RP SEQUENCE FROM N.A.
RC SPECIES=B.t.israelensis;
RX MEDLINE=87086764; PubMed=3025452;
RA Ward E.S., Ellar D.J.;
RT "Bacillus thuringiensis var. israelensis delta-endotoxin. Nucleotide
RT sequence and characterization of the transcripts in Bacillus
RT thuringiensis and Escherichia coli.";
RL J. Mol. Biol. 191:1-11(1986).
RN [2]
RP SEQUENCE FROM N.A.
RC SPECIES=B.t.israelensis;
RX MEDLINE=87086767; PubMed=3025453;
RA Ward E.S., Ridley A.R., Ellar D.J., Todd J.A.;
RT "Bacillus thuringiensis var. israelensis delta-endotoxin. Cloning and
RT expression of the toxin in sporogenic and asporogenic strains of
RT Bacillus subtilis.";
RL J. Mol. Biol. 191:13-22(1986).
RN [3]
RP SEQUENCE FROM N.A., AND MUTAGENESIS.
RC SPECIES=B.t.israelensis;
RX MEDLINE=89011977; PubMed=2845100;
RA Ward E.S., Ellar D.J., Chilcott C.N.;
RT "Single amino acid changes in the Bacillus thuringiensis var.
RT israelensis delta-endotoxin affect the toxicity and expression of the
RT protein.";
RL J. Mol. Biol. 202:527-535(1988).
RN [4]
RP SEQUENCE FROM N.A.
RC SPECIES=B.t.israelensis;
RX MEDLINE=86067227; PubMed=4070003;
RA Waalwijk C., Duilemans A.M., van Workum M.E.S., Visser B.;
RT "Molecular cloning and the nucleotide sequence of the Mr 28 000
RT crystal protein gene of Bacillus thuringiensis subsp. israelensis.";
RL Nucleic Acids Res. 13:8207-8217(1985).
RN [5]
RP REVISIONS TO 34-35.
RC SPECIES=B.t.israelensis;
RA Waalwijk C.;
RL Submitted (FEB-1986) to the EMBL/GenBank/DBJ databases.
RN [6]

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RP SEQUENCE FROM N.A.
RC SPECIES=B.t.morriisoni; STRAIN=PG14;
RX MEDLINE=87203386; PubMed=3575104;
RA Earp D.J., Ellar D.J.;
RT "Bacillus thuringiensis var. morriisoni strain PG14: nucleotide
sequence of a gene encoding a 27kDa crystal protein.";
RL Nucleic Acids Res. 15:3619-3619(1987).
RN [17]
RP SEQUENCE FROM N.A.
RC SPECIES=B.t.morriisoni; STRAIN=PG14;
RA Gajjar N.J., Sivaprasad N., Federici B.A.;
RT "Bacillus thuringiensis subsp. israelensis" and sequence analysis of the gene encoding
a 27.3-kilodalton cytolytic protein from Bacillus thuringiensis subsp.
morriisoni (PG-14).";
RL Curr. Microbiol. 16:171-177(1987).
RN [17]
CC -!- FUNCTION: Kills the larvae of dipteran insects by making pores in
the epithelial cell membrane of the insect midgut. Acts on
mosquitoes and black flies.
CC -!- DEVELOPMENTAL STAGE: The crystal protein is produced during
sporulation and is accumulated both as an inclusion and as part of
the spore coat.
CC -!- PTM: Active after proteolytic processing.
CC -!- SIMILARITY: Belongs to the cyt1/cyt2 endotoxin family.
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or send an email to license@isb-sib.ch).
CC
CC EMBL; X04338; CAA27868.1; -
CC EMBL; X03182; CAA26943.1; -
CC EMBL; Y00135; CAA68329.1; -
CC EMBL; M35968; ARA22553.1; -
CC FIC; A24044; A24044.
CC FIC; A27520; A27520.
CC HSP; Q04470; ICBY.
CC InterPro; IPR001615; Endotoxin_CytB.
CC Pfam; PF01338; Bac_thur_toxin; 1.
CC ProDom; PD009844; Endotoxin_CytB; 1.
KW Flaemid; Sporulation; Toxin.
FT VARIANT 82
SQ SEQUENCE 249 AA; 27341 MW; E661946298D3989A CRC64;
Query Match 39.1%; Score 456; DB 1; Length 249;
Best Local Similarity 45.6%; Pred. No. 1.3e-26;
Matches 99; Conservative 44; Mismatches 64; Indels 10; Gaps 5;
QY 5 RVITLTVPSS-SDVNYSEIYQV-APQYVQALTLAKYFQGAIF-----DGSTLRDFEFA 56
DB 25 RVITLRVEDPNEINLLSINEIDNPNYILQAIMLANAFQNALVPTSTDFGDLRFSPK 84
QY 57 LOIANDI-PQAAVNTLQVQGVQVSVMDIKVIDMKNVLSIVIDNKXFDQVTA 115
DB 85 LEIANTITPMGAVSVYDQVNTQNNQSVVMINKVLEVLKTVLGVALSQSVI-DQLTA 143
QY 116 TMTFTNLNSQSEAWFYFKEDAKHTSYNNILFAIQDEETGGVWATLPIAFDISVDIEK 175
DB 144 TMTFTNLNTQKNEAWIFGKGTANTNTNTYNNVLFQAIQNAQQTGGVWYCVFVGF 203
QY 176 EKVLFVTIKTENYAVTVKAINVVQALQSSRDSKVVD 212
DB 204 EQVLFETIQDSASVNNVQLKFAQPLVSSSQYPIAD 240
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ID O52298 PRELIMINARY; PRT; 157 AA.
AC O52298;
DT 01-JUN-1998 (TReMBLrel. 06, Created)
DT 01-JUN-1998 (TReMBLrel. 06, Last sequence update)

DT 01-OCT-2003 (TReMBLrel. 25, Last annotation update)
DE Cytolytic toxin (Fragment).
GN Name=Cyt2Ba;
OS Bacillus thuringiensis (subsp. tenebrionis).
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
OX NCBI_TaxID=1444;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=97355937; PubMed=9212418;
RA Guerschicoff A., Ugalde R.A., Rubinstein C.P.;
RT "Identification and characterization of a previously undescribed cyt
gene in Bacillus thuringiensis subsp. israelensis";
RL Appl. Environ. Microbiol. 63:2716-2721(1997).
DR EMBL; AF034926; AAB95384.1; -
DR HSP; Q04470; ICBY.
DR GO; GO:0005576; C:extracellular; IEA.
DR GO; GO:0009405; P:pathogenesis; IEA.
DR GO; GO:0042243; P:spore wall assembly (sensu Bacteria); IEA.
DR InterPro; IPR001615; Endotoxin_CytB.
DR Pfam; PF01338; Bac_thur_toxin; 1.
DR ProDom; PD009844; Endotoxin_CytB; 1.
FT NON_TER 1
FT NON_TER 157
SQ SEQUENCE 157 AA; 17716 MW; 7A00550DD3E8A124 CRC64;
Query Match 38.5%; Score 448; DB 2; Length 157;
Best Local Similarity 55.5%; Pred. No. 3e-26;
Matches 86; Conservative 32; Mismatches 37; Indels 0; Gaps 0;
QY 40 FQAGIDGSLRPFDEKALQIANDIPQAAVNTLQVQGVQVSVMDIKVIDMKNVLS 99
DB 3 FQAGIDPLTLNFFNKALQIANGLENAGVTGTINQSVIHQITIEVSMISQIKIIRSVLG 62
QY 100 IVIDNKKFWDQVTAITMTFTNLNSQSEAWFYFKEDAKHTSYNNILFAIQDEETGGV 159
DB 63 LVINSANFNWSVSAITMTFTNLNLEPQVDENIWNLSATQTSYFKILFSLQNETGRF 122
QY 160 MATLPIAFDISVDIEKVKLVFTIKTENYAVTVK 194
DB 123 MAILPIAFETVQVQKQLLFTIKDSARYEVGMK 157
RESULT 10
ID Q7BVD4 PRELIMINARY; PRT; 157 AA.
AC Q7BVD4;
DT 05-JUL-2004 (TReMBLrel. 27, Created)
DT 05-JUL-2004 (TReMBLrel. 27, Last sequence update)
DE Putative cytolytic toxin (Fragment).
OS Bacillus thuringiensis.
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
OX NCBI_TaxID=1428;
RN [1]
RP SEQUENCE FROM N.A.
RX STRAIN=4K3;
RA MEDLINE=97355937; PubMed=9212418;
RA Guerschicoff A., Ugalde R.A., Rubinstein C.P.;
RT "Identification and characterization of a previously undescribed cyt
gene in Bacillus thuringiensis subsp. israelensis";
RL Appl. Environ. Microbiol. 63:2716-2721(1997).
DR EMBL; AF022886; AAB87600.1; -
DR GO; GO:0005576; C:extracellular; IEA.
DR GO; GO:0009405; P:pathogenesis; IEA.
DR GO; GO:0042243; P:spore wall assembly (sensu Bacteria); IEA.
DR InterPro; IPR001615; Endotoxin_CytB.
DR Pfam; PF01338; Bac_thur_toxin; 1.
DR ProDom; PD009844; Endotoxin_CytB; 1.
FT NON_TER 1
FT NON_TER 157
SQ SEQUENCE 157 AA; 17716 MW; 7A00550DD3E8A124 CRC64;
Query Match 38.5%; Score 448; DB 2; Length 157;


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Matches 84; Conservative 32; Mismatches 36; Indels 0; Gaps 0;
QY 40 FQGAIDGSLRPFKALQIANDIPQAAVNTLNQTVQOQTVQVSMIDKIVIMKNVLS 99
DB 3 FQGAIDPLTLNFKALQIANGLNAGVTGTINQSVIHQITIEVSMWISQIKIIRSVLG 62
QY 100 IVIDNKKFVDQVTAATNTFTNLNSQSESEAWIFYKEDAHKTSYYNINILPAIDQETGGV 159
DB 63 LVINSANFNWVNSAINTFTNLEPQVDENWVNRNLSATQTSFYKILFSLQNETGRF 122
QY 160 MATLPIAFDISVDIEKELVFTIKDTENYAV 191
DB 123 MAILPIAFELTVDVQKQLLFTIKDSARYEV 154

RESULT 14
CXBA_BACTW
ID CXBA_BACTW STANDARD; PRT; 265 AA.
AC Q45790;
DT 15-JUL-1998 (Rel. 36, Created)
DT 05-JUL-1998 (Rel. 36, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Type-1Ba cytolytic delta-endotoxin.
GN Name-cyt1Ba;
OS Bacillus thuringiensis (subsp. neoleoensis).
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
OX NCBI_TaxID=43262;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=PS201T6;
RA Narva K.E., Payne J.M., Uyeda K.A., Stalder C.J., Michaels T.B.;
RL Submitted (JUL-1996) to the EMBL/GenBank/DBJ databases.
CC -!- FUNCTION: Kills the larvae of dipteran insects by making pores in
CC the epithelial cell membrane of the insect midgut (By similarity).
CC -!- DEVELOPMENTAL STAGE: The crystal protein is produced during
CC sporulation and is accumulated both as an inclusion and as part of
CC the spore coat.
CC -!- PTM: Active after proteolytic processing (By similarity).
CC -!- SIMILARITY: Belongs to the cyt1/cyt2 endotoxin family.
CC
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CC
CC EMBL; U37196; AAB03693.1; -.
CC HSSP; Q04470; ICBY.
CC InterPro; IPR001615; Endotoxin_CytB.
CC Pfam; PF01338; Bac thur toxin; 1.
CC ProDom; PD009844; Endotoxin_CytB; 1.
CC Sporulation; Toxin.
CC SEQUENCE 265 AA; 29906 MW; 260D1495F8C477A2 CRC64;
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CC Query Match 36.4%; Score 423.5; DB 1; Length 265;
CC Best Local Similarity 40.9%; Pred. No. 4.1e-24;
CC Matches 94; Conservative 47; Mismatches 72; Indels 17; Gaps 6;
QY 5 RVITLTVPSDDVVN---PQVNOALTLAKYFQGA- - - - -DGSLRPFDE 54
DB 38 RVILYLVK--KDPIDTTLLEITEIENPNVLAQIQLAAAFQDALVPTETEFGEAIRFSP 95
QY 55 KALQIANDI-PQAAVNTLNQTVQOQTVQVSMIDKIVIMKNVLSIVIDNKKFWDQVTA 113
DB 96 KGLEVAKTIQPGAVVAYTDQTSQSNQVSMIDRVISLVKTVMGVALSG-SITQLTA 154
QY 114 AITNTFTNLNSQSEAWIFYKEDAHKTSYYNINILPAIDQETGGVMTLPFAFDISVDI 173
DB 155 AITDFTNLNTQKDSANFPWKGKTHQNTYTNVNFPAIQNETGRVMVCVPIGFIRVFT 214
QY 174 EKEKVLFTIKDTENYAVTVKAINVVQALQSSRDSKVD---AFKSPRHL 220
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DB 215 DKRTVLFLTKDYANYSVNIQTLRFAQLIDSRALSINDLSALRSKYL 264

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AC P94594;
DT 15-JUL-1998 (Rel. 36, Created)
DT 15-JUL-1998 (Rel. 36, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Type-1ab cytolytic delta-endotoxin (27 kDa cytolytic toxin).
GN Name-cyt1Ab;
OS Bacillus thuringiensis (subsp. medellin).
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
OX NCBI_TaxID=79672;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=H30 / 163-131;
RX MEDLINE=97176379; PubMed=9023925;
RA Thierry I., Delecuse A., Tamayo M.C., Orduz S.;
RT Identification of a gene for Cyt1A-like hemolysin from Bacillus
RT thuringiensis subsp. medellin and expression in a crystal-negative B.
RT thuringiensis strain.
RL Appl. Environ. Microbiol. 63:468-473(1997).
CC -!- FUNCTION: Kills the larvae of dipteran insects by making pores in
CC the epithelial cell membrane of the insect midgut.
CC -!- DEVELOPMENTAL STAGE: The crystal protein is produced during
CC sporulation and is accumulated both as an inclusion and as part of
CC the spore coat.
CC -!- PTM: Active after proteolytic processing.
CC -!- SIMILARITY: Belongs to the cyt1/cyt2 endotoxin family.
CC
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CC or send an email to license@isb-sib.ch).
CC
CC EMBL; X98793; CAAG7328.1; -.
CC HSSP; Q04470; ICBY.
CC InterPro; IPR001615; Endotoxin_CytB.
CC Pfam; PF01338; Bac thur toxin; 1.
CC ProDom; PD009844; Endotoxin_CytB; 1.
CC Sporulation; Toxin.
CC SEQUENCE 250 AA; 27507 MW; A57464B0E2C7AEF6 CRC64;
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CC Best Local Similarity 41.4%; Pred. No. 1.3e-23;
CC Matches 91; Conservative 52; Mismatches 62; Indels 15; Gaps 6;
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DB 25 RVITLRIDDPNEINLLSINEIEN- - - - -NYLLQALANAFQKALVPTSTFEADALQFSM 82
QY 54 KALQIANDI-PQAAVNTLNQTVQOQTVQVSMIDKIVIMKNVLSIVIDNKKFWDQV 112
DB 83 TKGLEVANTISPPGAVQVQVQDNVSQTNQNSAMINKVLDLKSILGVAL-QGSVIEQT 141
QY 113 AAITNTFTNLNSQSEAWIFYKEDAHKTSYYNINILPAIDQETGGVMTLPFAFDISVD 172
DB 142 SAVTNTFTNLNTQKNEAMIFNGRETSTQNTYTNVNFPAIQNETGRVGVVCPVGFPEIKVS 201
QY 173 IEKEKVLFTIKDTENYAVTVKAINVVQALQSSRDSKVD 212
DB 202 AVKERVLTITQDSASYNVNIQSLKFAQPLVSASEYPIAD 241

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OM protein - protein search, using sw model

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Perfect score: 1165
Sequence: 1 MFNFRVITLTPSSDVVNVYS.....DAFKSPRLPRKHKICSNS 231

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Total number of hits satisfying chosen parameters: 1717557

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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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1	1165	100.0	231	14 US-10-386-972-2	Sequence 2, Appli
2	1165	100.0	231	16 US-10-767-605-2	Sequence 2, Appli
3	101	8.7	477	15 US-10-335-977-9400	Sequence 9400, Ap
4	97	8.3	1833	8 US-08-945-5670-4	Sequence 4, Appli
5	97	8.3	1833	8 US-08-621-944A-4	Sequence 4, Appli
6	97	8.3	1833	14 US-10-175-282-4	Sequence 4, Appli
7	97	8.3	1833	14 US-10-175-275-4	Sequence 4, Appli
8	97	8.3	1992	8 US-08-945-5670-3	Sequence 3, Appli
9	97	8.3	1992	8 US-08-621-944A-3	Sequence 3, Appli
10	97	8.3	1992	14 US-10-175-282-3	Sequence 3, Appli
11	97	8.3	1992	14 US-10-175-275-3	Sequence 3, Appli

12	95.5	8.2	421	15	US-10-282-122A-63417	Sequence 63417, A
13	95.5	8.2	1876	15	US-10-282-122A-73861	Sequence 73861, A
14	94.5	8.1	249	15	US-10-369-493-17326	Sequence 17326, A
15	94.5	8.1	356	15	US-10-424-599-317207	Sequence 217207, A
16	94	8.1	372	15	US-10-425-114-53891	Sequence 53891, A
17	94	8.1	383	15	US-10-425-114-59141	Sequence 59141, A
18	93	8.0	2122	9	US-09-813-214A-9	Sequence 9, Appli
19	92.5	7.9	4688	15	US-10-282-122A-76865	Sequence 76865, A
20	90	7.7	1280	15	US-10-452-024-139	Sequence 139, App
21	90	7.7	1280	15	US-10-452-024-140	Sequence 140, App
22	89.5	7.7	1278	15	US-10-452-024-152	Sequence 152, App
23	89.5	7.7	1278	15	US-10-205-516-12	Sequence 12, Appli
24	89.5	7.7	1288	15	US-10-205-516-26	Sequence 26, Appli
25	89.5	7.7	4961	14	US-10-114-153-64	Sequence 64, Appli
26	89	7.6	246	15	US-10-282-122A-53616	Sequence 53616, A
27	89	7.6	1101	16	US-10-437-963-172676	Sequence 172676, A
28	89	7.6	1389	17	US-10-732-923-17027	Sequence 17027, A
29	89	7.6	1805	10	US-09-820-843A-73	Sequence 73, Appli
30	89	7.6	1805	15	US-10-282-122A-63513	Sequence 63513, A
31	89	7.6	1805	17	US-10-732-923-3303	Sequence 3303, Ap
32	88.5	7.6	787	15	US-10-282-122A-72461	Sequence 72461, A
33	88	7.6	736	15	US-10-387-977-105	Sequence 105, App
34	87.5	7.5	935	16	US-10-478-451-7	Sequence 7, Appli
35	87.5	7.5	1087	17	US-10-732-923-8260	Sequence 8260, Ap
36	87	7.5	653	9	US-09-759-010-2	Sequence 2, Appli
37	87	7.5	653	16	US-10-408-765A-13	Sequence 13, Appli
38	87	7.5	911	14	US-10-032-585-7655	Sequence 7655, Ap
39	87	7.5	1170	16	US-10-437-963-107142	Sequence 107142, A
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41	86.5	7.4	474	14	US-10-127-032-100	Sequence 100, App
42	86.5	7.4	1300	9	US-09-815-242-4903	Sequence 4903, Ap
43	86.5	7.4	1300	9	US-09-815-242-10906	Sequence 10906, A
44	86.5	7.4	1418	15	US-10-369-493-22315	Sequence 22315, A
45	86.5	7.4	1903	17	US-10-766-993-3	Sequence 3, Appli

ALIGNMENTS

RESULT 1
US-10-386-972-2
; Sequence 2, Application US/10386972
; Publication NO. US20030167521A1
; GENERAL INFORMATION:
; APPLICANT: Rupa, Mark J.
; APPLICANT: Donovan, William P.
; APPLICANT: Tan, Yuping
; APPLICANT: Slaney, Amette C.
; TITLE OF INVENTION: Bacillus thuringiensis CryET29 Compositions Toxic to Coleopteran
; FILE REFERENCE: MECO:017--2
; CURRENT APPLICATION NUMBER: US/10/386,972
; PRIOR FILING DATE: 2003-03-12
; PRIOR APPLICATION NUMBER: 09/611,216
; PRIOR FILING DATE: 2000-07-06
; PRIOR APPLICATION NUMBER: 08/721,259
; PRIOR FILING DATE: 1996-09-26
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 2
; LENGTH: 231
; TYPE: PRT
; ORGANISM: Bacillus thuringiensis
US-10-386-972-2

Query Match 100.0%; Score 1165; DB 14; Length 231;
Best Local Similarity 100.0%; Pred. No. 2.6e-99;
Matches 231; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MFNFRVITLTPSSDVVNVYSIYVAPQVNVNQLTKYFQGAIDGTLRFDFEKALQIA 60
DB 1 MFNFRVITLTPSSDVVNVYSIYVAPQVNVNQLTKYFQGAIDGTLRFDFEKALQIA 60

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QY 61 NDIPQAAVNTLNQTVQGGTVQVSVMDKIVDMKNVLSIVIDNKKFWDQVTAATNTFT 120
Db 61 NDIPQAAVNTLNQTVQGGTVQVSVMDKIVDMKNVLSIVIDNKKFWDQVTAATNTFT 120
QY 121 NLNQSSEAWIFYPKEDAHKTSYYNIIILFAIQDEETGGVMATLPIAFDISVDIEKEKVL 180
Db 121 NLNQSSEAWIFYPKEDAHKTSYYNIIILFAIQDEETGGVMATLPIAFDISVDIEKEKVL 180
QY 181 VTIKTENYAVTVKAINVQALQSSRDSKVVDFAFKSPRHLPRKRHKICSNS 231
Db 181 VTIKTENYAVTVKAINVQALQSSRDSKVVDFAFKSPRHLPRKRHKICSNS 231

RESULT 2
US-10-767-605-2
; Sequence 2, Application US/10767605
; Publication No. US20040127695A1
; GENERAL INFORMATION:
; APPLICANT: Rutar, Mark J.
; APPLICANT: Donovan, William P.
; APPLICANT: Tan, Yiping
; APPLICANT: Slaney, Annette C.
; TITLE OF INVENTION: Plants Toxic to Coleopteran Insects and Ctenocephalides Spp.
; TITLE OF INVENTION: (Amended)
; FILE REFERENCE: MECO-017--3
; CURRENT APPLICATION NUMBER: US/10/767,605
; CURRENT FILING DATE: 2004-01-29
; PRIOR APPLICATION NUMBER: 10/386,972
; PRIOR FILING DATE: 2003-03-12
; PRIOR APPLICATION NUMBER: 09/611,216
; PRIOR FILING DATE: 2000-07-06
; PRIOR APPLICATION NUMBER: 08/721,259
; PRIOR FILING DATE: 1996-09-26
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 2
; TYPE: PR1
; ORGANISM: Bacillus thuringiensis
US-10-767-605-2

Query Match 100.0%; Score 1165; DB 16; Length 231;
Best Local Similarity 100.0%; Pred. No. 2.6e-99;
Matches 231; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MFFNRVITLTVPSSDVVNYSEIYQVAPQVNVQALTLAKYFQGAIDGSTLRDFEKAQIA 60
Db 1 MFFNRVITLTVPSSDVVNYSEIYQVAPQVNVQALTLAKYFQGAIDGSTLRDFEKAQIA 60
QY 61 NDIPQAAVNTLNQTVQGGTVQVSVMDKIVDMKNVLSIVIDNKKFWDQVTAATNTFT 120
Db 61 NDIPQAAVNTLNQTVQGGTVQVSVMDKIVDMKNVLSIVIDNKKFWDQVTAATNTFT 120
QY 121 NLNQSSEAWIFYPKEDAHKTSYYNIIILFAIQDEETGGVMATLPIAFDISVDIEKEKVL 180
Db 121 NLNQSSEAWIFYPKEDAHKTSYYNIIILFAIQDEETGGVMATLPIAFDISVDIEKEKVL 180
QY 181 VTIKTENYAVTVKAINVQALQSSRDSKVVDFAFKSPRHLPRKRHKICSNS 231
Db 181 VTIKTENYAVTVKAINVQALQSSRDSKVVDFAFKSPRHLPRKRHKICSNS 231

RESULT 3
US-10-335-977-9400
; Sequence 9400, Application US/10335977
; Publication No. US20040052799A1
; GENERAL INFORMATION:
; APPLICANT: DOUGLAS SMITH et al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES
; RELATING TO HELICOBACTER PYLORI FOR
; DIAGNOSTICS AND THERAPEUTICS
; NUMBER OF SEQUENCES: 10031
; CORRESPONDENCE ADDRESS:

QY 61 NDIPQAAVNTLNQTVQGGTVQVSVMDKIVDMKNVLSIVIDNKKFWDQVTAATNTFT 120
Db 61 NDIPQAAVNTLNQTVQGGTVQVSVMDKIVDMKNVLSIVIDNKKFWDQVTAATNTFT 120
QY 121 NLNQSSEAWIFYPKEDAHKTSYYNIIILFAIQDEETGGVMATLPIAFDISVDIEKEKVL 180
Db 121 NLNQSSEAWIFYPKEDAHKTSYYNIIILFAIQDEETGGVMATLPIAFDISVDIEKEKVL 180
QY 181 VTIKTENYAVTVKAINVQALQSSRDSKVVDFAFKSPRHLPRKRHKICSNS 231
Db 181 VTIKTENYAVTVKAINVQALQSSRDSKVVDFAFKSPRHLPRKRHKICSNS 231

RESULT 4
US-08-945-567D-4
; Sequence 4, Application US/08945567D
; Publication No. US20010014672A1
; GENERAL INFORMATION:
; APPLICANT: SASAKI, Ken
; APPLICANT: HARKNESS, Robin E.
; APPLICANT: LOOSMORE, Sheena M.
; APPLICANT: CHONG, Pele
; APPLICANT: KLEIN, Michel H.
; TITLE OF INVENTION: HIGH MOLECULAR WEIGHT MAJOR OUTER MEMBRANE PROTEIN OF
; MORAXELLA
; TITLE OF INVENTION: MORAXELLA
; FILE REFERENCE: 1038-745 MIS
```

```
; ADDRESSEE: LAHIVE & COCKFIELD
; STREET: 28 State Street
; CITY: Boston
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02109-1875
; COMPUTER READABLE FORM:
; MEDIUM TYPE: CD-ROM ISO9660
; COMPUTER: IBM PC Compatible
; OPERATING SYSTEM: Windows NT 4.0
; SOFTWARE: UNIX
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/335,977
; FILING DATE: 30-Dec-2002
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/993,002
; FILING DATE: 17-DEC-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Mandragouras, Amy E.
; REGISTRATION NUMBER: 36,207
; REFERENCE/DOCKET NUMBER: GTN-018
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617)227-7400
; TELEFAX: (617)742-4214
; INFORMATION FOR SEQ ID NO: 9400:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 477 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; HYPOTHEetical: YES
; ORIGINAL SOURCE:
; ORGANISM: Helicobacter pylori
; FEATURE:
; NAME/KEY: misc.feature
; LOCATION: (B) LOCATION 1...477
; SEQUENCE DESCRIPTION: SEQ ID NO: 9400:
US-10-335-977-9400

Query Match 8.7%; Score 101; DB 15; Length 477;
Best Local Similarity 20.1%; Pred. No. 1.4;
Matches 46; Conservative 55; Mismatches 90; Indels 38; Gaps 10;

QY 2 PFN---RVITITVP-----SSDVVNYSEIYQVAPQVNVQALTLAKYFQGAI---DGSITLRF 51
Db 199 YFNLMARMLAQKLEQIQTDIKRVTKLYDKGLTTDIDQLSKA--QGNLSYDILDMQF 256
QY 52 DFEKALQIANDIPQAAVNTLNQTVQGGTVQVSVMDKIVDMKNVLSIVIDNKKFWDQV 111
Db 257 ALEQNRLTLEVTNLSVQNLKKTITIDAPNLQRLERQD--LVSLREQISALRYQNKQL--- 311
QY 112 TAAITNTFTNLNQSSEAWIFYPKEDAHKTSYYNIIILFAIQDEETGGVMATLPIAFDISV 171
Db 312 ----NYPKIDVDS--WLEFIQKPAYATGRFGN--FVPGQONTAGVTATLNFDDIGL 362
QY 172 DIEKEKVLFTVIKOTENYA-----VTVKAINVQALQSSRDS 208
Db 363 SLQKQSIMLQGLANEKNLAYKKLEQKDEQLYRKSLLDARAKIESKAS 411

RESULT 4
US-08-945-567D-4
; Sequence 4, Application US/08945567D
; Publication No. US20010014672A1
; GENERAL INFORMATION:
; APPLICANT: SASAKI, Ken
; APPLICANT: HARKNESS, Robin E.
; APPLICANT: LOOSMORE, Sheena M.
; APPLICANT: CHONG, Pele
; APPLICANT: KLEIN, Michel H.
; TITLE OF INVENTION: HIGH MOLECULAR WEIGHT MAJOR OUTER MEMBRANE PROTEIN OF
; MORAXELLA
; TITLE OF INVENTION: MORAXELLA
; FILE REFERENCE: 1038-745 MIS
```

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; CURRENT APPLICATION NUMBER: US/08/945,567D
; CURRENT FILING DATE: 1996-04-29
; PRIOR APPLICATION NUMBER: 08/431,718
; PRIOR FILING DATE: 1995-05-01
; PRIOR APPLICATION NUMBER: 08/478,370
; PRIOR FILING DATE: 1995-06-07
; PRIOR APPLICATION NUMBER: 08/621,944
; PRIOR FILING DATE: 1996-03-26
; PRIOR APPLICATION NUMBER: PCT/CA96/00264
; PRIOR FILING DATE: 1996-04-29
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 4
; LENGTH: 1833
; TYPE: PRT
; ORGANISM: Moraxella catarrhalis
US-08-945-567D-4

Query Match      8.3%; Score 97; DB 8; Length 1833;
Best Local Similarity 22.8%; Pred. No. 20;
Matches 50; Conservative 40; Mismatches 93; Indels 36; Gaps 7;

QY 13 SSDVNVSEIYQVAPQYVNVQALTLAKYFQGAIDGSLRDFEKAQIAN-----61
Db 898 SHDAVTGGKIYDLKTELENKISSHTAKQNSLHEFSVADEQGNFTVSNPYSSYDTSKTS 957
QY 62 DIPQAAVNTLNQTVQOQTVQVSVNMIDKIVDIMK-----NVLISVIDNKKFMDQVTAI 115
Db 958 DVIITFAGENGITTKVNGVVRGIDQTKGLTTPKLTGVNNGKGIVDSQNGQNTIT-GL 1016
QY 116 TMTFTNLMSQSEAMIFYKEDAHKTSYYNLFIAQDEE---TGGVMATLPIAFDISVD 172
Db 1017 SNTLANVTNDKGSV-----RTTEQGNI---IKDEDKTRAASIVDVLVSAGFNLOQN 1063
QY 173 IEKEKVLFTIKDTENYAVTVKAINVQALQSSRDSKV 211
Db 1064 --GEAVDFVSTYDTVNFADGNATTAKVTYDDTSKTSKV 1100

RESULT 5
US-08-621-944A-4
; Sequence 4, Application US/08621944A
; Publication No. US2002068070A1
; GENERAL INFORMATION:
; APPLICANT: SASAKI, Ken
; APPLICANT: HARKNESS, Robin E.
; APPLICANT: LOOSMORE, Sheena M.
; APPLICANT: KLEIN, Michel H.
; TITLE OF INVENTION: HIGH MOLECULAR WEIGHT MAJOR OUTER
; TITLE OF INVENTION: MEMBRANE PROTEIN OF MORAXELLA
; NUMBER OF SEQUENCES: 10
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Sim & McBurney
; STREET: Suite 701, 330 University Avenue
; CITY: Toronto
; STATE: Ontario
; COUNTRY: Canada
; ZIP: M5G 1R7
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/621,944A
; FILING DATE: 26-MAR-1996
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/478,370
; FILING DATE: 07-JUN-1995
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Stewart, Michael I

; REGISTRATION NUMBER: 24,973
; REFERENCE/DOCKET NUMBER: 1038-587
; TELEPHONE: (416) 595-1155
; TELEFAX: (416) 595-1163
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1833 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
US-08-621-944A-4

Query Match      8.3%; Score 97; DB 8; Length 1833;
Best Local Similarity 22.8%; Pred. No. 20;
Matches 50; Conservative 40; Mismatches 93; Indels 36; Gaps 7;

QY 13 SSDVNVSEIYQVAPQYVNVQALTLAKYFQGAIDGSLRDFEKAQIAN-----61
Db 898 SHDAVTGGKIYDLKTELENKISSHTAKQNSLHEFSVADEQGNFTVSNPYSSYDTSKTS 957
QY 62 DIPQAAVNTLNQTVQOQTVQVSVNMIDKIVDIMK-----NVLISVIDNKKFMDQVTAI 115
Db 958 DVIITFAGENGITTKVNGVVRGIDQTKGLTTPKLTGVNNGKGIVDSQNGQNTIT-GL 1016
QY 116 TMTFTNLMSQSEAMIFYKEDAHKTSYYNLFIAQDEE---TGGVMATLPIAFDISVD 172
Db 1017 SNTLANVTNDKGSV-----RTTEQGNI---IKDEDKTRAASIVDVLVSAGFNLOQN 1063
QY 173 IEKEKVLFTIKDTENYAVTVKAINVQALQSSRDSKV 211
Db 1064 --GEAVDFVSTYDTVNFADGNATTAKVTYDDTSKTSKV 1100

RESULT 6
US-10-175-282-4
; Sequence 4, Application US/10175282
; Publication No. US20030170657A1
; GENERAL INFORMATION:
; APPLICANT: SASAKI, Ken
; APPLICANT: HARKNESS, Robin E.
; APPLICANT: LOOSMORE, Sheena M.
; APPLICANT: CHONG, Pele
; APPLICANT: KLEIN, Michel H.
; TITLE OF INVENTION: HIGH MOLECULAR WEIGHT MAJOR OUTER MEMBRANE PROTEIN OF
; FILE REFERENCE: 1038-1234 MIS
; CURRENT APPLICATION NUMBER: US/10/175,282
; CURRENT FILING DATE: 2002-06-20
; PRIOR APPLICATION NUMBER: 08/945,567
; PRIOR FILING DATE: 1998-03-19
; PRIOR APPLICATION NUMBER: 08/431,718
; PRIOR FILING DATE: 1995-05-01
; PRIOR APPLICATION NUMBER: 08/478,370
; PRIOR FILING DATE: 1995-06-07
; PRIOR APPLICATION NUMBER: 08/621,944
; PRIOR FILING DATE: 1996-03-26
; PRIOR APPLICATION NUMBER: PCT/CA96/00264
; PRIOR FILING DATE: 1996-04-29
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 4
; LENGTH: 1833
; TYPE: PRT
; ORGANISM: Moraxella catarrhalis
US-10-175-282-4

Query Match      8.3%; Score 97; DB 14; Length 1833;
Best Local Similarity 22.8%; Pred. No. 20;
Matches 50; Conservative 40; Mismatches 93; Indels 36; Gaps 7;

QY 13 SSDVNVSEIYQVAPQYVNVQALTLAKYFQGAIDGSLRDFEKAQIAN-----61
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Db 898 SHDAVTGKGYDLTKTELENKISSHTAKTAQNSLHFEVSVADEQGNFTVSNPYSSYDTSKTS 957
Qy 62 DIPQAAVNTLNQTVQOQTVQSVNMIDKIVDIMK-----NVLSIVIDNKKFWDQVTAAI 115
Db 958 DVITPAGENGITTKVNGKGVVRGIDQTKGLTTPKLTGVNNGKGVIDSQNGQNTIT-GL 1016
Qy 116 TMTFTNLNSQSEAWIFYKEDAKHTSYVYNILFAIQDEE---TGGVWATLPIAFDISVD 172
Db 1017 SNTLANVTNDKGSV-----RTTEQGNM-----IKDEKTRAASIVDVLVSAGFNLOQN 1063

Qy 173 IEKEKVLFTVTKDTEYAVTVKAINVVQALQSSRDSKV 211
Db 1064 --GEAVDFVSTYDTVNFADGNATTAKVYDDTSKTSKV 1100

RESULT 7
US-10-175-275-4
; Sequence 4, Application US/10175275
; Publication No. US20030171254A1
; GENERAL INFORMATION:
; APPLICANT: SASAKI, Ken
; APPLICANT: HARKNESS, Robin E.
; APPLICANT: LOOSMORE, Sheena M.
; APPLICANT: CHONG, Pele
; APPLICANT: KLEIN, Michel H.
; TITLE OF INVENTION: HIGH MOLECULAR WEIGHT MAJOR OUTER MEMBRANE PROTEIN OF
; FILE REFERENCE: 1038-1235 MIS
; CURRENT APPLICATION NUMBER: US/10/175,275
; CURRENT FILING DATE: 2002-06-20
; PRIOR APPLICATION NUMBER: 2002-06-20
; PRIOR FILING DATE: 1998-03-19
; PRIOR FILING DATE: 1995-05-01
; PRIOR FILING DATE: 1995-06-07
; PRIOR FILING DATE: 1996-03-26
; PRIOR FILING DATE: 1996-04-29
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: Patent In Ver. 2.1
; SEQ ID NO 4
; LENGTH: 1833
; TYPE: PRT
; ORGANISM: Moraxella catarrhalis
US-10-175-275-4

Query Match 8.3%; Score 97; DB 14; Length 1833;
Best Local Similarity 22.8%; Pred. No. 20;
Matches 50; Conservative 40; Mismatches 93; Indels 36; Gaps 7;

Qy 13 SSDVVNYSEIYQVAPQVYNQALTLAKYFQGAIDGSLRDFEKAQIAN-----61
Db 898 SHDAVTGKGYDLTKTELENKISSHTAKTAQNSLHFEVSVADEQGNFTVSNPYSSYDTSKTS 957
Qy 62 DIPQAAVNTLNQTVQOQTVQSVNMIDKIVDIMK-----NVLSIVIDNKKFWDQVTAAI 115
Db 958 DVITPAGENGITTKVNGKGVVRGIDQTKGLTTPKLTGVNNGKGVIDSQNGQNTIT-GL 1016
Qy 116 TMTFTNLNSQSEAWIFYKEDAKHTSYVYNILFAIQDEE---TGGVWATLPIAFDISVD 172
Db 1017 SNTLANVTNDKGSV-----RTTEQGNM-----IKDEKTRAASIVDVLVSAGFNLOQN 1063

Qy 173 IEKEKVLFTVTKDTEYAVTVKAINVVQALQSSRDSKV 211
Db 1064 --GEAVDFVSTYDTVNFADGNATTAKVYDDTSKTSKV 1100

RESULT 8
US-08-945-567D-3
; Sequence 3, Application US/08945567D
; Publication No. US20010014672A1
```

```
; GENERAL INFORMATION:
; APPLICANT: SASAKI, Ken
; APPLICANT: HARKNESS, Robin E.
; APPLICANT: LOOSMORE, Sheena M.
; APPLICANT: CHONG, Pele
; APPLICANT: KLEIN, Michel H.
; TITLE OF INVENTION: HIGH MOLECULAR WEIGHT MAJOR OUTER MEMBRANE PROTEIN OF
; FILE REFERENCE: 1038-745 MIS
; CURRENT APPLICATION NUMBER: US/08/945,567D
; CURRENT FILING DATE: 1996-04-29
; PRIOR APPLICATION NUMBER: 08/431,718
; PRIOR FILING DATE: 1995-05-01
; PRIOR APPLICATION NUMBER: 08/478,370
; PRIOR FILING DATE: 1995-06-07
; PRIOR APPLICATION NUMBER: 08/621,944
; PRIOR FILING DATE: 1996-03-26
; PRIOR APPLICATION NUMBER: PCT/CA96/00264
; PRIOR FILING DATE: 1996-04-29
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: Patent In Ver. 2.1
; SEQ ID NO 3
; LENGTH: 1992
; TYPE: PRT
; ORGANISM: Moraxella catarrhalis
US-08-945-567D-3

Query Match 8.3%; Score 97; DB 8; Length 1992;
Best Local Similarity 22.8%; Pred. No. 23;
Matches 50; Conservative 40; Mismatches 93; Indels 36; Gaps 7;

Qy 13 SSDVVNYSEIYQVAPQVYNQALTLAKYFQGAIDGSLRDFEKAQIAN-----61
Db 1057 SHDAVTGKGYDLTKTELENKISSHTAKTAQNSLHFEVSVADEQGNFTVSNPYSSYDTSKTS 1116
Qy 62 DIPQAAVNTLNQTVQOQTVQSVNMIDKIVDIMK-----NVLSIVIDNKKFWDQVTAAI 115
Db 1117 DVITPAGENGITTKVNGKGVVRGIDQTKGLTTPKLTGVNNGKGVIDSQNGQNTIT-GL 1175
Qy 116 TMTFTNLNSQSEAWIFYKEDAKHTSYVYNILFAIQDEE---TGGVWATLPIAFDISVD 172
Db 1176 SNTLANVTNDKGSV-----RTTEQGNM-----IKDEKTRAASIVDVLVSAGFNLOQN 1222

Qy 173 IEKEKVLFTVTKDTEYAVTVKAINVVQALQSSRDSKV 211
Db 1223 --GEAVDFVSTYDTVNFADGNATTAKVYDDTSKTSKV 1259

RESULT 9
US-08-621-944A-3
; Sequence 3, Application US/08621944A
; Publication No. US20020068070A1
; GENERAL INFORMATION:
; APPLICANT: SASAKI, Ken
; APPLICANT: HARKNESS, Robin E.
; APPLICANT: LOOSMORE, Sheena M.
; APPLICANT: KLEIN, Michel H.
; TITLE OF INVENTION: HIGH MOLECULAR WEIGHT MAJOR OUTER
; NUMBER OF SEQUENCES: 10
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Sim & McBurney
; STREET: Suite 701, 330 University Avenue
; CITY: Toronto
; STATE: Ontario
; COUNTRY: Canada
; ZIP: M5G 1R7
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
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APPLICATION NUMBER: US/08/621,944A
FILING DATE: 26-MAR-1996
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/478,370
FILING DATE: 07-JUN-1995
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Stewart, Michael I
REGISTRATION NUMBER: 24,973
REFERENCE/DOCKET NUMBER: 1038-587
TELECOMMUNICATION INFORMATION:
TELEPHONE: (416) 595-1155
TELEFAX: (416) 595-1163
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 1992 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-621-944A-3

Query Match 8.3%; Score 97; DB 8; Length 1992;
Best Local Similarity 22.8%; Pred. No. 23;
Matches 50; Conservative 40; Mismatches 93; Indels 36; Gaps 7;
QY 13 SSDVNNYSIYQVAPQYVNOALTAKYFQGAIDGSLRFDPEKALQIAN-----61
DB 1057 SHDAVTGGKIYDLKTELENKISSAKTQNSLHFSVADEQGNFTVSNPYSSYDTSKTS 1116
QY 62 DIPQAAVNTLNQTVQOQTVQVSMIDKIVDIMK-----NVLSTVIDNKKFWDQVTAI 115
DB 1117 DVITFAGENGITTKVNGVVRVIGIDQTKGLTPKLTGVNNGKGVIVDSQNGQNTIT-GL 1175
QY 116 TMTFTNLNSQSEAWIFYKEDAHKTSYYNILFAIQDEE---TGGWATLPIAFDISVD 172
DB 1176 SNTLANVTNDKGSV-----RTTEQGNI---IKDEKTRAASIVDVLVSAGFNLOGN 1222
QY 173 IEKEKLVFTIKDTENYAVTVKAINVQALQSSRSKVV 211
DB 1223 --GEAVDFVSTYDTVNFADGNATTAKVTYDDTSKTSKVV 1259

RESULT 10
US-10-175-282-3
Sequence 3, Application US/10175282
Publication No. US20030170657A1
GENERAL INFORMATION:
APPLICANT: SASAKI, Ken
APPLICANT: HARKNESS, Robin E.
APPLICANT: LOOSMORE, Sheena M.
APPLICANT: CHONG, Pele
APPLICANT: KLEIN, Michel H.
TITLE OF INVENTION: HIGH MOLECULAR WEIGHT MAJOR OUTER MEMBRANE PROTEIN OF
FILE REFERENCE: 1038-1234 MIS
CURRENT APPLICATION NUMBER: US/10/175,282
PRIOR FILING DATE: 2002-06-20
PRIOR APPLICATION NUMBER: 08/945,567
PRIOR FILING DATE: 1998-03-19
PRIOR APPLICATION NUMBER: 08/431,718
PRIOR FILING DATE: 1995-05-01
PRIOR APPLICATION NUMBER: 08/478,370
PRIOR FILING DATE: 1995-06-07
PRIOR APPLICATION NUMBER: 08/621,944
PRIOR FILING DATE: 1996-03-26
PRIOR APPLICATION NUMBER: PCT/CA96/00264
NUMBER OF SEQ ID NOS: 10
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 3
LENGTH: 1992
TYPE: PRT

ORGANISM: Moraxella catarrhalis
US-10-175-282-3
Query Match 8.3%; Score 97; DB 14; Length 1992;
Best Local Similarity 22.8%; Pred. No. 23;
Matches 50; Conservative 40; Mismatches 93; Indels 36; Gaps 7;
QY 13 SSDVNNYSIYQVAPQYVNOALTAKYFQGAIDGSLRFDPEKALQIAN-----61
DB 1057 SHDAVTGGKIYDLKTELENKISSAKTQNSLHFSVADEQGNFTVSNPYSSYDTSKTS 1116
QY 62 DIPQAAVNTLNQTVQOQTVQVSMIDKIVDIMK-----NVLSTVIDNKKFWDQVTAI 115
DB 1117 DVITFAGENGITTKVNGVVRVIGIDQTKGLTPKLTGVNNGKGVIVDSQNGQNTIT-GL 1175
QY 116 TMTFTNLNSQSEAWIFYKEDAHKTSYYNILFAIQDEE---TGGWATLPIAFDISVD 172
DB 1176 SNTLANVTNDKGSV-----RTTEQGNI---IKDEKTRAASIVDVLVSAGFNLOGN 1222
QY 173 IEKEKLVFTIKDTENYAVTVKAINVQALQSSRSKVV 211
DB 1223 --GEAVDFVSTYDTVNFADGNATTAKVTYDDTSKTSKVV 1259

RESULT 11
US-10-175-275-3
Sequence 3, Application US/10175275
Publication No. US20030171254A1
GENERAL INFORMATION:
APPLICANT: SASAKI, Ken
APPLICANT: HARKNESS, Robin E.
APPLICANT: LOOSMORE, Sheena M.
APPLICANT: CHONG, Pele
APPLICANT: KLEIN, Michel H.
TITLE OF INVENTION: HIGH MOLECULAR WEIGHT MAJOR OUTER MEMBRANE PROTEIN OF
FILE REFERENCE: 1038-1235 MIS
CURRENT APPLICATION NUMBER: US/10/175,275
CURRENT FILING DATE: 2002-06-20
PRIOR APPLICATION NUMBER: 08/945,567
PRIOR FILING DATE: 1998-03-19
PRIOR APPLICATION NUMBER: 08/431,718
PRIOR FILING DATE: 1995-05-01
PRIOR APPLICATION NUMBER: 08/478,370
PRIOR FILING DATE: 1995-06-07
PRIOR APPLICATION NUMBER: 08/621,944
PRIOR FILING DATE: 1996-03-26
PRIOR APPLICATION NUMBER: PCT/CA96/00264
NUMBER OF SEQ ID NOS: 10
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 3
LENGTH: 1992
TYPE: PRT
ORGANISM: Moraxella catarrhalis
US-10-175-275-3

Query Match 8.3%; Score 97; DB 14; Length 1992;
Best Local Similarity 22.8%; Pred. No. 23;
Matches 50; Conservative 40; Mismatches 93; Indels 36; Gaps 7;
QY 13 SSDVNNYSIYQVAPQYVNOALTAKYFQGAIDGSLRFDPEKALQIAN-----61
DB 1057 SHDAVTGGKIYDLKTELENKISSAKTQNSLHFSVADEQGNFTVSNPYSSYDTSKTS 1116
QY 62 DIPQAAVNTLNQTVQOQTVQVSMIDKIVDIMK-----NVLSTVIDNKKFWDQVTAI 115
DB 1117 DVITFAGENGITTKVNGVVRVIGIDQTKGLTPKLTGVNNGKGVIVDSQNGQNTIT-GL 1175
QY 116 TMTFTNLNSQSEAWIFYKEDAHKTSYYNILFAIQDEE---TGGWATLPIAFDISVD 172
DB 1176 SNTLANVTNDKGSV-----RTTEQGNI---IKDEKTRAASIVDVLVSAGFNLOGN 1222

RESULT 14
US-10-369-493-17326
; Sequence 17326, Application US/10369493
; Publication No. US20030233675A1
; GENERAL INFORMATION:
; APPLICANT: Cao, Yongwei
; APPLICANT: Hinkle, Gregory J.
; APPLICANT: Slater, Steven C.
; APPLICANT: Goldman, Barry S.
; APPLICANT: Chen, Xianfeng
; TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF
; FILE REFERENCE: 38-10(52052)B
; CURRENT APPLICATION NUMBER: US/10/369,493
; CURRENT FILING DATE: 2003-02-28
; PRIOR APPLICATION NUMBER: US 60/360,039
; PRIOR FILING DATE: 2002-02-21
; NUMBER OF SEQ ID NOS: 47374
; SEQ ID NO 17326
; LENGTH: 249
; TYPE: PRT
; ORGANISM: Bacillus halodurans
US-10-369-493-17326

Query Match 8.1%; Score 94.5; DB 15; Length 249;
Best Local Similarity 21.0%; Pred. No. 2.3;
Matches 37; Conservative 38; Mismatches 64; Indels 37; Gaps 7;
QY 62 DIPQAAVNTLNQTVQGVVSMI-----DKIVDMKNVLSIVIDNKKFWDQVTAI 115
DB 8 DVGKVRPHNEDGTIMKNGQLLVVADGMGHHQAGDVASKWATELL--KEAWSEAS--- 62
QY 116 TMTFTNLNSQSEAMIFYFKEDAHKTSYYYNILFAIQDEETGGVMATLPIAFDISVDIEK 175
DB 63 ----LSPSSQSEGLRNQVLHVNSLHY----AQKHECQGMGTTL-----VAAIVDK 109
QY 176 EKVLFTTKDNTENYAVTVKAINVVOALQSSRDSKVVDAP-----KSPRHLPRK 223
DB 110 ERVTIAHIGDSRAYLLNEHGPS-----QKTRDHSVLNVLRTGQISDBEAHHPRK 160

RESULT 15
US-10-424-599-217207
; Sequence 217207, Application US/10424599
; Publication No. US20040031072A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J
; APPLICANT: Kovalic, David K
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated with
; FILE REFERENCE: 38-21(53223)B
; CURRENT APPLICATION NUMBER: US/10/424,599
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 285684
; SEQ ID NO 217207
; LENGTH: 356
; TYPE: PRT
; ORGANISM: Glycine max
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT3847_38165C.1.pap
US-10-424-599-217207

Query Match 8.1%; Score 94.5; DB 15; Length 356;
Best Local Similarity 20.7%; Pred. No. 3.7;
Matches 58; Conservative 39; Mismatches 114; Indels 69; Gaps 10;
QY 5 RVITLTVFSSDV-----VNYSEIYQVAPQVNVQALTLAKYF----- 40
DB 74 RALIITABKNIPWRKMAQEILESEVYRELESIQNSQLVYPDYLYNPFHAYERGLNLTWL 133

QY 41 ---QGAIDGSTL-----RPFDEKALQIANDIPOAAVNTLNQTVQGVVSMIDKIVDIM 94
DB 134 AAEEAAATILMARRAPFDASSLOEANKILRGNWLTANNHHMQ--YSESCVDDILDI- 190
QY 95 KNVLSIVIDNKKFWDQV-TAAIT-----NTFTNLNSQSESE-----AWIFYFKEDA- 138
DB 191 --GCSVGIGISTRYLADKFPPTAKVTGFEMSSYFVAVNQKQERAMPKRPFIKNIHANGEDTV 248
QY 139 --HKTSSYYNIFAIQDEET-----GGVMATLPIAFDISVDIEKVKVLF 180
DB 249 LPSKSFDLVLSIAFVLHECPTRVIVNLVREAPRLLRPGGTALTDFSLKSKVLQELSPVLF 308
QY 181 VTIKDTENYAVTVKAINVVOALQSSRDSKVVDAPFKSPRHL 220
DB 309 TLVKSSTPFLDEYILTDMDETLREAGFVNITSILTDPRHV 348

Search completed: June 26, 2005, 16:09:50
Job time : 160 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: June 26, 2005, 15:47:02 ; Search time 162 Seconds
(without alignments)
551.492 Million cell updates/sec

Title: US-10-767-605-2
Perfect score: 1165
Sequence: 1 MFNRVITLTPSSDVVNS.....DAFKSPRLPRKHKICSNS 231

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 2105692

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq_16Dec04:*
1: Geneseqp1980s:*
2: Geneseqp1990s:*
3: Geneseqp2000s:*
4: Geneseqp2001s:*
5: Geneseqp2002s:*
6: Geneseqp2003as:*
7: Geneseqp2003bs:*
8: Geneseqp2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1151	98.8	231	2 AAW55027	Aaw55027 Bacillus
2	457	39.2	249	2 AAR10282	Aar10282 Mutant 27
3	456	39.1	249	2 AAR04831	Aar04831 Bacillus
4	451	38.7	249	2 AAR10853	Aar10853 Mutant 27
5	450	38.6	249	2 AAR10283	Aar10283 Mutant 27
6	450	38.6	249	2 AAR10309	Aar10309 Mutant 27
7	442.5	38.0	220	2 AAR24023	Aar24023 Anticance
8	424	36.4	218	1 AAP90062	Aap90062 Peptide w
9	423.5	36.4	265	2 AAR70754	Aar70754 Delta-end
10	423.5	36.4	265	2 AAR91966	Aar91966 PS201T6 3
11	423.5	36.4	265	2 AAW07850	Aaw07850 Delta-end
12	423.5	36.4	265	2 AAY01207	Aay01207 B. thurin
13	417	35.8	222	2 AAR70755	Aar70755 Delta-end
14	417	35.8	222	2 AAR91967	Aar91967 Truncated
15	417	35.8	222	2 AAY01208	Aay01208 B. thurin
16	415.5	35.7	265	3 AAB03646	Aab03646 CytC tox
17	103	8.8	401	5 ABUS1322	Abus1322 Helicobac
18	103	8.8	415	5 ABUS2179	Abus2179 Helicobac
19	101	8.7	477	2 AAY10993	Aay10993 H. pylori
20	100	8.6	210	5 ABUS1679	Abus1679 Helicobac
21	97	8.3	1992	4 AAW04505	Aaw04505 Moraxella
22	97	8.3	1992	4 AAB69137	Aab69137 M. catarr
23	97	8.3	1992	4 AAB69133	Aab69133 M. catarr
24	97	8.3	2047	4 AAB69134	Aab69134 M. catarr
25	96.5	8.3	201	4 AAB59843	Aab59843 AcMNPV OR

26	95.5	8.2	421	6	ABU35493	Abu35493 Protein e
27	95.5	8.2	1876	6	ABU45937	Abu45937 Protein e
28	94.5	8.1	249	8	ADS28293	Adse28293 Bacterial
29	94.5	8.1	393	6	ABR53069	AbR53069 Protein s
30	94.5	8.1	393	7	ADK62078	Adk62078 Disease t
31	93	8.0	2122	6	ABU08784	Abu08784 Moraxella
32	93	8.0	2123	4	AAE00701	Aae00701 Moraxella
33	92.5	7.9	192	5	ABU51662	Abu51662 Helicobac
34	92.5	7.9	4688	6	ABU48941	Abu48941 Protein e
35	92	7.9	2053	4	AAB69135	Aab69135 M. catarr
36	90	7.7	293	6	ABM73470	Abm73470 Staphyloc
37	89.5	7.7	1059	3	AAU93309	Aau93309 A mangane
38	89.5	7.7	1084	3	AAU93312	Aau93312 A mangane
39	89.5	7.7	4903	6	ABU12072	Abu12072 Human NOV
40	89.5	7.7	4913	8	ADH72246	Adh72246 Human pro
41	89.5	7.7	4961	8	ADH72236	Adh72236 Human pro
42	89	7.6	157	5	ABU50735	Abu50735 Helicobac
43	89	7.6	182	5	ABU52262	Abu52262 Helicobac
44	89	7.6	246	6	ABU25692	Abu25692 Protein e
45	89	7.6	373	7	ADF07179	Adf07179 Bacterial

ALIGNMENTS

RESULT 1
AAW55027
ID AAW55027 standard; protein; 231 AA.

AC AAW55027;

DT 16-SEP-1998 (first entry)

DE Bacillus thuringiensis CryET29 protein.

KW Bacillus thuringiensis; CryET29; crystal protein; Japanese beetle;

KW Southern corn rootworm; Western corn rootworm; Colorado potato beetle;

KW red flour beetle; cat flea; transgenic plant; insecticide.

OS Bacillus thuringiensis.

PN WO9813497-A1.

PD 02-APR-1998.

PF 25-SEP-1997; 97WO-US017507.

PR 26-SEP-1996; 96US-00721259.

XX (ECOG-) ECOGEN INC.

Rupar MJ, Donovan WP, Tan Y, Slaney AC;

WPI; 1998-230707/20.

N-PSDB; AAV271172.

New Bacillus thuringiensis CryET29 crystal protein - having activity

against e.g. Southern corn rootworm, Colorado potato beetle, Japanese

beetle, red flour beetle and cat fleas.

Claim 2; Fig 1; 101pp; English.

The CryET29 crystal protein has activity against the Southern corn rootworm, Western corn rootworm, Colorado potato beetle, Japanese beetle and red flour beetle and also against fleas, in particular larvae of the cat flea, Ctenocephalides felis. CryET29 can therefore be used to prevent infestations by these insects. The gene can be used to produce transgenic plants which express the toxic proteins and therefore insecticidal activity against pests

SQ Sequence 231 AA;

Query Match 98.8%; Score 1151; DB 2; Length 231;

Best Local Similarity 99.1%; Pred. No. 9.4e-104;
Matches 229; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 MFFNRVITLTPSSDVVNSYIYQVAPQVYVNOALTAKYFQGAIDGSLRDFEFKALQIA 60
Db 1 MFFNRVITLTPSSDVVNSYIYQVAPQVYVNOALTAKYFQGAIDGSLRDFEFKALQIA 60

Qy 61 NDIPOAAVNTLNQTVQGGTVQVSMIDKIYDIMKNVLSIVIDNKKFWDQVTAITNTFT 120
Db 61 NDIPOAAVNTLNQTVQGGTVQVSMIDKIYDIMKNVLSIVIDNKKFWDQVTAITNTFT 120

Qy 121 NLNQSSEAWIFPKYKEDAHKTSYYNIIFAIQDEBTGGVMATLPIAFDISVDIEKVLV 180
Db 121 NLNQSSEAWIFPKYKEDAHKTSYYNIIFAIQDEBTGGVMATLPIAFDISVDIEKVLV 180

Qy 181 VTIKDTENYAVTVKAINVVQALQSSRSKVVDAFKSPRHLPRKRHKICSNS 231
Db 181 VTIKDTENYAVTVKAINVVQALQSSRSKVVDAFKSPRHLPRKRHKICSNS 231

RESULT 2
ID AAR10282 standard; protein; 249 AA.
AC AAR10282;
XX 04-APR-1991 (first entry)
DT Mutant 27kD delta endotoxin.
DE Mutant delta endotoxin; insecticide; mosquitoes; chimeric protein.
KW Mutant delta endotoxin.
XX Bacillus thuringiensis.
OS US000875-H.
XX 01-JAN-1991.
PD 18-MAR-1988; 88US-00170211.
XX 18-MAR-1988; 88US-00170211.
PR (DUPO) DU PONT DE NEMOURS & CO E I.
PA Ellar DJ, Ward ES;
PI WPI; 1991-028850/04.
DR Nucleic acid fragments encoding mutant 27 kD delta endotoxins - from
XX Bacillus thuringiensis var. israelensis, have improved insecticidal
PT properties, part. against mosquitoes.
XX Disclosure; Fig 1; 14pp; English.

This mutant 27 kD delta endotoxin has a single amino acid substit- ution
(Arg-30 to Ala) in the wild-type sequence. This results in a soluble
insecticidal protein with improved insecticidal properties, e.g. lower
haemolytic activity and greater expression in cells contg. sig. ants. of
phosphatidate-type toxin receptors. It is hence useful e.g. against
mosquitoes. See also AAR10853, AAR10283 and AAR10309

Sequence 249 AA;
Query Match 39.2%; Score 457; DB 2; Length 249;
Best Local Similarity 45.6%; Pred. No. 5.4e-36;
Matches 99; Conservative 44; Mismatches 36; Indels 10; Gaps 5;

Qy 5 RVITLTPSS-SDVVNSYIYQV-APQVYVNOALTAKYFQGAIDGSLRDFEFK 56
Db 25 RVITLTPSS-SDVVNSYIYQV-APQVYVNOALTAKYFQGAIDGSLRDFEFK 84

Qy 57 LQIANDI-POAAVNTLNQTVQGGTVQVSMIDKIYDIMKNVLSIVIDNKKFWDQVTAI 115
Db 57 LQIANDI-POAAVNTLNQTVQGGTVQVSMIDKIYDIMKNVLSIVIDNKKFWDQVTAI 115

Db 85 LEIANTITPMGAVVSYVDQNTQNNQVSMINKVLELVKTVLGVLSGSGVI-DQLTA 143
Qy 116 TMTNTNLSQSEAWIFPKYKEDAHKTSYYNIIFAIQDEBTGGVMATLPIAFDISVDIEK 175
Db 144 TMTNTNLSQSEAWIFPKYKEDAHKTSYYNIIFAIQDEBTGGVMATLPIAFDISVDIEK 203

Qy 176 EKVLFTVTKDTENYAVTVKAINVVQALQSSRSKVV 212
Db 204 EKVLFTVTKDTENYAVTVKAINVVQALQSSRSKVV 240

RESULT 3
ID AAR04831 standard; protein; 249 AA.
XX AAR04831;
XX 25-MAR-2003 (revised)
DT 25-SEP-1989 (first entry)
XX Bacillus thuringiensis var. israelensis 27kD crystal protein.
DE Crystal protein; insecticide; Diptera.
KW Bacillus thuringiensis.
XX US4918006-A.
XX 17-APR-1990.
XX 03-FEB-1986; 86US-00824912.
XX 01-JUL-1985; 85US-00750211.
PR (DUPO) DU PONT DE NEMOURS & CO E I.
PA Ellar DJ, Ward ES;
PI WPI; 1990-156076/20.
DR N-PSDB; AAQ04456.
XX Gene coding for Bacillus thuringiensis var. israelensis crystal protein -
PT used to express insecticidal protein active esp. against order Diptera in
PT larval form.
XX Disclosure; Page ?; -pp; English.

This is the sequence of a protein toxin with a mol.wt. of 27D which is
homologous to the 26-28D protein present in crystal of B.thuringiensis
var. israelensis. The protein is toxic to insect pests esp. Diptera (eg
larvae of mosquitoes and blackflies) and used, either in its entirety or
as an insecticidally effective fragment, as an insecticide. (Updated on
25-MAR-2003 to correct PA field.)

Sequence 249 AA;
Query Match 39.1%; Score 456; DB 2; Length 249;
Best Local Similarity 45.6%; Pred. No. 6.8e-36;
Matches 99; Conservative 44; Mismatches 64; Indels 10; Gaps 5;

Qy 5 RVITLTPSS-SDVVNSYIYQV-APQVYVNOALTAKYFQGAIDGSLRDFEFK 56
Db 25 RVITLTPSS-SDVVNSYIYQV-APQVYVNOALTAKYFQGAIDGSLRDFEFK 84

Qy 57 LQIANDI-POAAVNTLNQTVQGGTVQVSMIDKIYDIMKNVLSIVIDNKKFWDQVTAI 115
Db 85 LEIANTITPMGAVVSYVDQNTQNNQVSMINKVLELVKTVLGVLSGSGVI-DQLTA 143

Qy 116 TMTNTNLSQSEAWIFPKYKEDAHKTSYYNIIFAIQDEBTGGVMATLPIAFDISVDIEK 175
Db 144 TMTNTNLSQSEAWIFPKYKEDAHKTSYYNIIFAIQDEBTGGVMATLPIAFDISVDIEK 203

Qy 176 EKVLFTVTKDTENYAVTVKAINVVQALQSSRSKVV 212

PN US000875-H.
XX 01-JAN-1991.
XX 18-MAR-1988; 88US-00170211.
XX 18-MAR-1988; 88US-00170211.
XX (DUPO) DU PONT DE NEMOURS & CO E I.
XX Ellar DJ, Ward ES;
XX WPI; 1991-028850/04.
XX Nucleic acid fragments encoding mutant 27 KD delta endotoxins - from
PT Bacillus thuringiensis var. israelensis, have improved insecticidal
PT properties, part. against mosquitoes.
XX Disclosure; Fig 1; 14pp; English.
XX This mutant 27 kd delta endotoxin has a single amino acid substit- ution
CC (Lys-124 to Ala) in the wild-type sequence. This results in a soluble
CC insecticidal protein with improved insecticidal properties, e.g. lower
CC haemolytic activity and greater expression in cells contg. sig. ants. of
CC phosphatidate-type toxin receptors. It is hence useful e.g. against
CC mosquitoes. See also AAR10853 and AAR10282-83
XX Sequence 249 AA;
SQ Query Match 38.6%; Score 450; DB 2; Length 249;
Best Local Similarity 45.2%; Pred. No. 2.6e-35;
Matches 98; Conservative 44; Mismatches 65; Indels 10; Gaps 5;
Qy 5 RVITLTVPSS-SDVNNYSIYQV-APQYVNOALTILAKYFQGA------DGSTLRDFEKA
Db 25 RVITLRVEDPNEINLLSINEIDNPYILQAIMLANAFONALVPTSTDFGDALRFSMPKG 84
Qy 57 LOIANDI-PQAAVNTLNQTVQGVSVVMIDKIVDMKNVLSIVIDNKKFWDQVTAI 115
Db 85 LEIANTITPMGAVSVYDQNTQTNNQVSVMNKVLVLTATLVGVALSGSVI-DQLTAAV 143
Qy 116 TMTFTNLNSQSEAWIFYKEDAKHTSYNNILFAIQDEETGGVMATLPIAFDISVDIEK 175
Db 144 TMTFTNLNTQNEAWIFMGKETANTQNTYTNVLFPAIQNAQTGGVMYCVPGVFEIKVSAVK 203
Qy 176 EKVLFVTIKTENYAVTVKAINVVQALQSSRDSKVVD 212
Db 204 EQVLFFTIQDSASYNVNIQSLKFAQPLVSSSTQYPIAD 240
RESULT 7
AAR24023
ID AAR24023 standard; peptide; 220 AA.
AC AAR24023;
XX 25-NOV-1992 (first entry)
XX Anticancer agent.
XX Thermochemotherapy; Bacillus thuringiensis.
XX Bacillus sp.
XX JP04128240-A.
XX 28-APR-1992.
XX 03-SEP-1990; 90JP-00232943.
XX 25-JUN-1990; 90JP-00166071.
XX (TONG) TOA GOSEI CHEM IND LTD.

XX WPI; 1992-190107/23.
XX Anticancer agent for thermo-chemotherapy - contains polypeptide produced
PT from bacillus, and is pref. used with phloeomycin.
XX Disclosure; Fig 1; 5pp; Japanese.
XX The sequence given is an anticancer agent for thermochemotherapy and has
CC a molecular weight of 25000. This protein is very efficient esp. when
CC used together with phloeomycin and chemotherapy. This anticancer agent
CC is pref. isolated from Bacillus thuringiensis
XX Sequence 220 AA;
SQ Query Match 38.0%; Score 442.5; DB 2; Length 220;
Best Local Similarity 44.9%; Pred. No. 1.2e-34;
Matches 93; Conservative 44; Mismatches 61; Indels 9; Gaps 4;
Qy 14 SDVNNYSIYQV-APQYVNOALTILAKYFQGA------DGSTLRDFEKAQIANDI-PQ 65
Db 6 NEINLLSINEIDNPYILQAIMLANAFONALVPTSTDFGDALRFSMPKGLEIANTITPM 65
Qy 66 AAVNTLNQTVQGVSVVMIDKIVDMKNVLSIVIDNKKFWDQVTAI-TNTFTNLNSQ 125
Db 66 GAVSVYDQNTQTNNQVSVMNKVLVLTATLVGVALSGSVI-DQLTAAV-TNTFTNLNTQ 124
Qy 126 ESEAWIFYKEDAKHTSYNNILFAIQDEETGGVMATLPIAFDISVDIEKSKVLFVTIKD 185
Db 125 KNEAWIFMGKETANTQNTYTNVLFPAIQNAQTGGVMYCVPGVFEIKVSAVKEQVLFFTIQD 184
Qy 186 TENYAVTVKAINVVQALQSSRDSKVVD 212
Db 185 SASYNVNIQSLKFAQPLVSSSTQYPIAD 211
RESULT 8
AAP90062
ID AAP90062 standard; peptide; 218 AA.
XX AAP90062;
AC AAP90062;
XX 24-OCT-2003 (revised)
DT 25-MAR-2003 (revised)
DT 09-AUG-1990 (first entry)
XX Peptide with anticancer activity.
XX Anticancer agent; enhancer.
XX Bacillus thuringiensis serovar israelensis; ONR-60A.
XX JP01104019-A.
XX 21-APR-1989.
XX 29-JUL-1988; 88JP-00188207.
XX 31-JUL-1987; 87JP-00190347.
XX (TOAG) TOA GOSEI CHEM IND LTD.
XX WPI; 1989-161673/22.
XX Anticancer agents - contain polypeptide enhancer produced by Bacillus
PT microorganism.
XX Claim 1; Fig 6; 7pp; Japanese.
XX The polypeptide has anticancer activity and is capable of synergistically
CC enhancing other agents such as bleomycin, adriamycin, 5-FU and esp.
CC neocarzinostatin and thio-TEPA. See also J01104018. (Updated on 25-MAR-
CC 2003 to correct PF field.) (Updated on 24-OCT-2003 to standardise OS

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CC field)
XX
SQ Sequence 218 AA;

Query Match          36.4%; Score 424; DB 1; Length 218;
Best Local Similarity 44.8%; Pred. No. 7.5e-33;
Matches 90; Conservative 44; Mismatches 57; Indels 10; Gaps 5;

Qy 14 SDVYNYSEIQV-APQYVNQALTLAKYFQGAI-----DGSTLRFDFEKAQIANDI-PQ 65
   : : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
Db 6 NEINLLSINEIDNPNTILQAIMLANAFONALVPVTSTDFGDALRFSMPKGLSIANTITPM 65

Qy 66 AAVVNTLNQTVOGQTVGVSVSMIDKIIVIMKNVLISVIDNKKFWDQVTAATNTPTNLNSQ 125
   : : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
Db 66 GAVSYVDHVHTQTNN-QVSVMINKVLEVLTKVLGVALSGSVI-DQLTAAVNTTFTNLNTQ 123

Qy 126 ESEAWIFVYKEDANKTSYYNILFAIODEETGGVYNATLPFAFDISVDIEKEKVLPVTIKD 185
   : : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
Db 124 KNEAWIFWGETANQTNTYTNLVLFPAIONAQOTGGVNYCPVGFEIKVSANVEQVLFFTIQD 183

Qy 186 TENYAVTVKAINVVQALQSSR 206
   : : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
Db 184 SASYNVNIQSILKFAQPLVSSQ 204

RESULT 9
AAR70754
ID AAR70754 standard; protein; 265 AA.
XX
AC AAR70754;
XX
DT 16-OCT-2003 (revised)
DT 25-MAR-2003 (revised)
DT 15-AUG-1995 (first entry)
XX
Delta-endotoxin 201T6.
DE XX
KW Delta-endotoxin; crystal protein; insecticide; pesticide;
KW biological control agent; pest control; yellow fever mosquito;
KW Aedes aegypti; housefly; Musca domestica; leafmining fly;
KW Liriomyza trifolii; Western corn rootworm; Diabrotica virgifera;
KW dipteran insect.
XX
OS Bacillus thuringiensis; var. neoleoensis.
XX
PN WO9502693-A1.
XX
PD 26-JAN-1995.
XX
PF 14-JUL-1994; 94WO-US007887.
XX
PR 15-JUL-1993; 93US-00093199.
PR 30-SEP-1993; 93US-00129610.
XX
(MYCO ) MYCOGEN CORP.
XX
Payne J, Narva KE, Uyeda KA, Stalder CJ, Michaels TE;
XX
WPI; 1995-067337/09.
DR N-PSDB; AAQ85261.
XX
Delta endotoxins produced by Bacillus thuringiensis isolates - are active
against dipteran and/or corn rootworm.
XX
Claim 3; Page 32-33; 38pp; English.
XX
DNA encoding a novel 30 kDa delta-endotoxin, 201T6 toxin, was isolated
from a gene library of Bacillus thuringiensis PS01T6 (NRRL B-18750) in
lambda Gem-11. Removal of the 43 N-terminal amino acids of the toxin gave
a 25 kDa toxin (AAR70755) of increased scope and potency. Recombinant
CC hosts expressing the toxin gene are used for biological control of insect
pests. (Updated on 25-MAR-2003 to correct PN field.) (Updated on 16-OCT-
CC 2003 to standardise OS field)

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Query Match 36.4%; Score 423.5; DB 2; Length 265;
 Best Local Similarity 40.9%; Pred. No. 1.1e-32;
 Matches 94; Conservative 47; Mismatches 72; Indels 17; Gaps 6;

QY 5 RVITLTPSSDVVNYSEIYQVA---POYVNOALTAKYFOGAI-----DGSTLRDPDE 54
 DB 38 RVIYLVK--KPIDTTQLLEITEIENPNYVLAQIAAFAQDALVPTTEFEGEAIRFSMP 95
 QY 55 KALQIANDI-POAAVNTLNQTVQGVSVMDIKVIDIMKNVLSIVIDNKKFWDQVTA 113
 DB 96 KGLEVAKTIQPGAVAVYTDQTLSSNNQVSMIDRVISVLKTMGVVALSG-SIITQLTA 154
 QY 114 AITWTFNLNSQSEAWIFYKKEDAHKTSYYVNIILFAIQDEETGVMATLPIAFDISVDI 173
 DB 155 AITDTFTNLNTQKDSAWFWMGKTSYHQNTYTNVNFALQNETTGRVMMCVPIGEIRVFT 214
 QY 174 EKEKVLFTVTKDNTENYAVTVKAINVVQALQSSRDSKVVD---AFKSPRHL 220
 DB 215 DKRTVLFITTKDYANYSVNIQTLEFAQPLIDSRALSINDLSEALRSSKYL 264

RESULT 11
 ID AA07850
 XX AA07850 standard; protein; 265 AA.

AC AA07850;
 XX
 DT 17-OCT-2003 (revised)
 DT 27-AUG-1997 (first entry)
 XX
 DE Delta-endotoxin.
 XX
 KW Delta-endotoxin; Bacillus thuringiensis; gram-positive bacteria; mirid;
 KW spore forming bacteria; parasporal crystalline protein; Lygus hesperus;
 KW hemipteran insect; insect pest; crop pest; leaf bug; Lygus lineolaris;
 KW pesticide.
 XX
 OS Bacillus thuringiensis; strain PS20176.

XX Key Location/Qualifiers
 FH Misc-difference 1..43
 FT /note= "removed to create activated truncated endotoxin"
 FT Protein 44..265
 FT /note= "mature activated delta-endotoxin"
 FT
 PN WO9639843-A1.
 XX
 PD 19-DEC-1996.

XX
 PF 07-JUN-1996; 96WO-US009987.
 XX
 PR 07-JUN-1995; 95US-00475924.
 XX
 PA (MYCO) MYCOGEN CORP.
 XX
 PI Stockhoff B, Conlan C;
 XX
 DR WPI; 1997-051641/05.
 DR N-PSDB; AAT47253.

XX Biological control of hemipteran insect pests - using Bacillus
 PT thuringiensis delta-endotoxin, pref. expressed by transformed plants.
 XX
 PS Disclosure; Page 19-20; 28pp; English.
 XX
 CC This sequence represents the delta-endotoxin of Bacillus thuringiensis
 CC (B.t.) isolate PS20176. B.t. is a gram-positive, spore forming bacterium
 CC characterised by parasporal crystalline protein inclusions. The proteins
 CC can be highly toxic to pests and are specific in their toxic activity,
 CC and include the delta-endotoxins. The crystalline toxins are generally
 CC recognised as being protoxins, requiring either particular physicochemical
 CC conditions or the action of certain proteases to generate an active

CC toxin. This protein sequence is activated by the removal of 43 N-terminal
 CC amino acids. The protein can be used in the method of the invention. The
 CC method of the invention is for controlling hemipteran insect pests. The
 CC method comprises the administration of a B.t. delta-endotoxin to the
 CC pests or their environment. Of the hemipteran insect pests, the mirids
 CC (including Lygus) are the most notorious crop pests. The endotoxin
 CC encoded by this sequence is especially useful for controlling the leaf
 CC bugs Lygus hesperus and L. lineolaris. The method provides an
 CC environmentally acceptable alternative to the use of chemical pesticides.
 CC (Updated on 17-OCT-2003 to standardise OS field)

XX Sequence 265 AA;

Query Match 36.4%; Score 423.5; DB 2; Length 265;
 Best Local Similarity 40.9%; Pred. No. 1.1e-32;
 Matches 94; Conservative 47; Mismatches 72; Indels 17; Gaps 6;

QY 5 RVITLTPSSDVVNYSEIYQVA---POYVNOALTAKYFOGAI-----DGSTLRDPDE 54
 DB 38 RVIYLVK--KPIDTTQLLEITEIENPNYVLAQIAAFAQDALVPTTEFEGEAIRFSMP 95
 QY 55 KALQIANDI-POAAVNTLNQTVQGVSVMDIKVIDIMKNVLSIVIDNKKFWDQVTA 113
 DB 96 KGLEVAKTIQPGAVAVYTDQTLSSNNQVSMIDRVISVLKTMGVVALSG-SIITQLTA 154
 QY 114 AITWTFNLNSQSEAWIFYKKEDAHKTSYYVNIILFAIQDEETGVMATLPIAFDISVDI 173
 DB 155 AITDTFTNLNTQKDSAWFWMGKTSYHQNTYTNVNFALQNETTGRVMMCVPIGEIRVFT 214
 QY 174 EKEKVLFTVTKDNTENYAVTVKAINVVQALQSSRDSKVVD---AFKSPRHL 220
 DB 215 DKRTVLFITTKDYANYSVNIQTLEFAQPLIDSRALSINDLSEALRSSKYL 264

RESULT 12
 AAY01207
 ID AAY01207 standard; protein; 265 AA.

XX AC AAY01207;
 AC
 DT 20-MAR-2003 (revised)
 DT 25-MAY-1999 (first entry)
 XX
 DE B. thuringiensis PS20176 30kd delta-endotoxin.
 XX
 KW Hemipteran; insect; pest; Bacillus thuringiensis; delta-endotoxin;
 KW Lygus hesperus; Lygus lineolaris; insecticide; chemical pesticide;
 KW insect management; insecticide resistance.

XX Bacillus thuringiensis.

XX US5885963-A.

XX 23-MAR-1999.

XX 07-JUN-1996; 96US-00657579.

XX 07-JUN-1995; 95US-00475924.

XX (MYCO) MYCOGEN CORP.

XX Conlan C, Stockhoff B;

XX WPI; 1999-228582/19.

XX N-PSDB; AAX26294.

XX New method of killing hemipteran insect pests - by administration of a
 PT Bacillus thuringiensis delta-endotoxin from the B. thuringiensis isolate
 PT PS12331, deposited in NRRL B-21011.

XX Example; Col 15-16; 10pp; English.

XX The invention relates to killing hemipteran insect pests by administering

CC a *Bacillus thuringiensis* delta-endotoxin from *B. thuringiensis* isolate
 CC PS123D1, deposited in NRRL B-21011. The hemipteran insect pests that can
 CC be controlled by this toxin are specifically Lygus hesperus and Lygus
 CC lineolaris. The method provides an alternative to control of hemipteran
 CC pests with chemical pesticides, allowing more environmentally-friendly
 CC insect management and provides a tool for management of insecticide
 CC resistance. The present sequence represents an approximately 30KD delta-
 CC endotoxin of *B. thuringiensis* isolate PS201T6. (Updated on 20-MAR-2003 to
 CC correct PF field.)
 XX
 SQ Sequence 265 AA;

Query Match 36.4%; Score 423.5; DB 2; Length 265;
 Best Local Similarity 40.9%; Pred. No. 1.1e-32;
 Matches 94; Conservative 47; Mismatches 72; Indels 17; Gaps 6;
 QY 5 RVITLTPSSDVVNSEIYQVA----PQVNOALTAKYFOGAI-----DGLTLRFDFPE 54
 DB 38 RVILYLV--KPIDITTLQLEITEIENPNVQLQIAAFAQDALVPTETEFGEAIRFSMP 95
 QY 55 KALQIANDI-POAAVNTLNQTVQGGTVQVSMIDKIVDIMKNVLSIVIDNKKFWDQVTA 113
 DB 96 KGLEVAKTIPKGVAVYTDQTLQSNNQVSMIDRVISVLKTVMGVALSG-SIITQLTA 154
 QY 114 AITNFTNLNSQSEAWIFYKEDAKHTSYNNILFAIQDEBTGGVMATLPIAFDISVDI 173
 DB 155 AITDFTNLNTQKDSAWFWGKETSHQNTYNNVMPAIQNETTGRVMCMVPIGFEIRVFT 214
 QY 174 EKEKVLFTVTKDTENYAVTVKAINVVOALQSSRDSKVVD---AFKSPRHL 220
 DB 215 DKRTVLFTTKDYANYSVNIQTLRPAQLIDSRALSINDLSEALRSSKYL 264

RESULT 13

AAR70755
 ID AAR70755 standard; protein; 222 AA.

XX AC AAR70755;

XX DT 16-OCT-2003 (revised)
 XX DT 25-MAR-2003 (revised)
 XX DT 15-AUG-1995 (first entry)

XX DE Delta-endotoxin 201T6 truncation.

XX KW Delta-endotoxin; crystal protein; insecticide; pesticide;
 KW biological control agent; pest control; yellow fever mosquito;
 KW *Aedes aegypti*; housefly; *Musca domestica*; leafmining fly;
 KW *Liriomyza trifolii*; Western corn rootworm; *Diabrotica virgifera*;
 KW dipteran insect.

XX OS *Bacillus thuringiensis*; var. *neoleoensis*.

XX PN WO9502693-A1.

XX PD 26-JAN-1995.

XX PF 14-JUL-1994; 94WO-US007887.

XX PR 15-JUL-1993; 93US-00093199.

XX PR 30-SEP-1993; 93US-00129610.

XX PA (MYCO) MYCOGEN CORP.

XX PI Payne J, Narva KE, Uyeda KA, Stalder CJ, Michaels TE;

XX DR WPI; 1995-067337/09.

XX DR N-PSDB; AAQ85261.

XX PT Delta endotoxins produced by *Bacillus thuringiensis* isolates - are active
 PT against dipteran and/or corn rootworm.

XX PS Claim 5; Page 33-34; 38pp; English.

XX

CC DNA encoding a novel 30 kDa delta-endotoxin, 201T6 toxin, was isolated
 CC from a gene library of *Bacillus thuringiensis* PS01T6 (NRRL B-18750) in
 CC lambda Gem-11. Removal of the 43 N-terminal amino acids of the toxin gave
 CC a 25 kDa toxin (AAR70755) of increased scope and potency. Recombinant
 CC hosts expressing the toxin gene are used for biological control of insect
 CC pests. (Updated on 25-MAR-2003 to correct PN field.) (Updated on 16-OCT-
 CC 2003 to standardise OS field.)
 XX
 SQ Sequence 222 AA;

Query Match 35.8%; Score 417; DB 2; Length 222;
 Best Local Similarity 41.9%; Pred. No. 3.7e-32;
 Matches 91; Conservative 42; Mismatches 72; Indels 12; Gaps 5;

QY 15 DVVNTSEIYQVA-POVNVQALTAKYFOGAI-----DGLTLRFDFPEKALQIANDI-POA 66
 DB 6 DTTQLLEITEIENPNVQLQIAAFAQDALVPTETEFGEAIRFSMPKGLEVAKTIPKG 65
 QY 67 AVVNTLNQTVQGGTVQVSMIDKIVDIMKNVLSIVIDNKKFWDQVTAATNTFTNLNSQE 126
 DB 66 AVVAVTDQTLQSNNQVSMIDRVISVLKTVMGVALSG-SIITQLTAATITDFTNLNTQK 124
 QY 127 SEAWIFYKEDAKHTSYNNILFAIQDEBTGGVMATLPIAFDISVDIEKELFVTIKDT 186
 DB 125 DSAMFWGKETSHQNTYNNVMPAIQNETTGRVMCMVPIGFEIRVFTDKRTVLFTTKDY 184
 QY 187 ENYAVTVKAINVVOALQSSRDSKVVD---AFKSPRHL 220
 DB 185 ANYSVNIQTLRPAQLIDSRALSINDLSEALRSSKYL 221

RESULT 14

AAR91967

ID AAR91967 standard; protein; 222 AA.

XX AC AAR91967;

XX DT 16-OCT-2003 (revised)
 XX DT 25-MAR-2003 (revised)
 XX DT 18-JUL-1996 (first entry)

XX DE Truncated PS201T6 30 kDa toxin.

XX KW Toxin; *Bacillus thuringiensis*; PS201T6; cockroach; insecticide.

XX OS *Bacillus thuringiensis*; isolate PS201T6.

XX PN US5489432-A.

XX PD 06-FEB-1996.

XX PF 30-SEP-1993; 93US-00129609.

XX PR 06-NOV-1991; 91US-00788654.

XX PR 19-OCT-1992; 92US-00958551.

XX PA (MYCO) MYCOGEN CORP.

XX PI Schnepf HE, Brower DO, Kennedy MK, Payne JM, Randall JB;

XX DR WPI; 1996-115589/12.

XX DR N-PSDB; AAT16027.

XX PT New purified toxin active against cockroaches - produced by a culture of
 PT *Bacillus thuringiensis* isolate PS201T6, has a mol. wt. less than 31 kD.

XX PS Claim 1; Col 19-22; 12pp; English.

XX CC This sequence represents a truncated form of the 30 kDa *Bacillus*
 CC *thuringiensis* (B.t.) toxin (see AAR91966), which is active against
 CC cockroaches. The encoding sequence was obtained from the B.t. isolate
 CC PS201T6, using the primers represented by AAT16031 and AAT16032. The

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OM protein - protein search, using sw model

Run on: June 26, 2005, 15:56:03 ; Search time 40 Seconds
(without alignments)
555.652 Million cell updates/sec

Title: US-10-767-605-2
Perfect score: 1165
Sequence: 1 MFNFRVILTVSPSSDVVNS.....DAFKSPRLPRKHKICSNS 231

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues
Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR 79:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	637	54.7	259	2 S32432	toxin cytB - Bacil
2	456	39.1	249	2 A27520	28K crystal protei
3	456	39.1	249	2 A24044	28K parasporal cry
4	103	8.8	477	2 E64595	hypothetical prote
5	101	8.7	477	2 F71918	hypothetical prote
6	99.5	8.5	4540	2 T30838	cytoplasmic dynein
7	96.5	8.3	343	2 A41874	transcription repr
8	95.5	8.2	201	2 A34146	hypothetical prote
9	95.5	8.2	421	1 F64205	thymidine phosphor
10	95.5	8.2	1876	2 E97944	zinc metalloprotei
11	94.5	8.1	249	2 A33963	hypothetical prote
12	94.5	8.1	393	2 S69708	26S proteasome reg
13	92.5	7.9	4688	2 F82885	hypothetical prote
14	91	7.8	458	2 E65068	hypothetical prote
15	89.5	7.7	311	2 T32776	hypothetical prote
16	89.5	7.7	1363	2 C84346	hypothetical prote
17	89	7.6	772	1 JQ2026	outer layer protei
18	89	7.6	1017	2 D90550	hypothetical prote
19	89	7.6	1389	2 T41230	hypothetical TPR d
20	89	7.6	1805	1 A64224	hypothetical prote
21	88.5	7.6	717	2 T28247	ORP MSV086 probab
22	88.5	7.6	735	2 D70174	methyl-accepting c
23	88.5	7.6	1447	2 F82909	hypothetical prote
24	88	7.6	458	2 E91092	probable invasion
25	88	7.6	458	2 A85938	probable invasion
26	88	7.6	646	2 A41587	bacteriophage prot
27	87.5	7.5	1636	2 S60403	probable membrane
28	87	7.5	390	2 S54026	ribosomal protein
29	87	7.5	488	2 T33739	hypothetical prote

30	87	7.5	653	2 A29821	dnak-type molecula
31	87	7.5	853	2 G90559	trse-like protein
32	86.5	7.4	382	2 A48492	polyaaccharide exp
33	86.5	7.4	474	2 G83507	flagellar capping
34	86.5	7.4	1418	2 S64918	hypothetical prote
35	86	7.4	739	2 H75001	hypothetical prote
36	86	7.4	1237	2 AC1583	methyl-accepting c
37	86	7.4	1595	2 T31082	internalin protein
38	85.5	7.3	518	2 F86814	endo-1,4-beta-xyla
39	85.5	7.3	1465	2 A70199	bifunctional purin
40	85.5	7.3	1648	2 S57163	hypothetical prote
41	85.5	7.3	2599	2 P90608	probable membrane
42	85	7.3	236	2 D84969	ABC transporter pe
43	85	7.3	320	2 F69527	basal-body rod mod
44	85	7.3	537	2 A35400	ISA1214-6 transpos
45	85	7.3	640	2 T03754	surface protein T6
					hypothetical prote

ALIGNMENTS

RESULT 1

S32432
toxin cytB - Bacillus thuringiensis
C:Species: Bacillus thuringiensis
C:Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 09-Jul-2004
C:Accession: S32432; S31476
R:Koni, P.A.; Ellar, D.J.
J: Mol. Biol. 229, 319-327, 1993
A:Title: Cloning and characterization of a novel Bacillus thuringiensis cytolytic delta
A:Reference number: S32432; MUID:93156045; PMID:8429550
A:Accession: S32432
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-259 <KON>
A:Cross-references: UNIPROT:Q04470; EMBL:Z14147; NID:G49305; PIDN:CAA78519.1; PID:G49307
C:Genetics:
A:Gene: cytB
C:Superfamily: 28K parasporal crystal protein

Query Match	54.7%	Score 637;	DB 2;	Length 259;
Best Local Similarity	56.0%	Pred. No. 1.2e-43;		
Matches 126;	Conservative 43;	Mismatches 54;	Indels 2;	Gaps 2;
QY	7	ITLTVPSDDVNSIYVAPQYVNOALTLAKYFQGAIDGSLRFPDFEKALQIANDIPOA	66	
Db	31	IVLTVPSSDLNFWTVFVQPOYINQALHLANAFQGAIDPLNLFNFEEKALQIANGIPNS	90	
QY	67	AVVNTLNTVQGGTVQVSMIDKIYDIMKNVLSIVIDNKKFWDQVTAATNTFTNLNSQE	126	
Db	91	AIVKTLNQSVIQQTVEISVMVVEQLKKIIQEVGLVINSTFWNSVEATIKGTFTNLDTOI	150	
QY	127	SEAWTFYKEDAKHTSYNYNLFALQDEETGCGMATLPADFISVDIEKEKULFVTIKOT	186	
Db	151	DEAWTFWHSLSAHTSYNYNLFISQNEBTDGAVMAVLPLAFESVDVEKQKLVFTIKDS	210	
QY	187	ENYAVTVKAINVQALQSRDSKVVDAFK-SPRHLPRKHKICSN	230	
Db	211	ARYEVKMAKTLVQALHSS-NAPIVDIFNNVNYLYSHNHKLIQN	254	

RESULT 2

A27520
28K crystal protein - Bacillus thuringiensis plasmide
N:Alternate names: 28K cytolytic protein; delta-endotoxin
C:Species: Bacillus thuringiensis
C:Date: 19-Nov-1988 #sequence_revision 19-Nov-1988 #text_change 09-Jul-2004
C:Accession: A27520; S06430
R:Earp, D.J.; Ellar, D.J.
Nucleic Acids Res. 15, 3619, 1987
A:Title: Bacillus thuringiensis var. morrisoni strain PG14: nucleotide sequence of a ge
A:Reference number: A27520; MUID:87203386; PMID:3575104
A:Accession: A27520

A;Molecule type: DNA
A;Residues: 1-249 <EAB>
A;Cross-references: UNIPROT:P05069; GB:Y00135; NID:g40260; PIDN:CAA68329.1; PID:g40261
A;Experimental source: strain morrisoni Pg14, 140kb plasmid
R:Galjart, N.J.; Sivasekaran, N.; Federici, B.A.
Curr. Microbiol. 16, 171-177, 1987
A;Title: Plasmid location, cloning, and sequence analysis of the gene encoding a 27.3-kDa
A;Reference number: S06430
A;Accession: S06430
A;Molecule type: DNA
A;Residues: 1-249 <GAL>
A;Cross-references: EMBL:M35968; NID:gi43104; PIDN:AAA22553.1; PID:gi43105
C;Genetics:
A;Genome: plasmid
C;Superfamily: 28k parasporal crystal protein
C;Keywords: delta-endotoxin

Query Match 39.1%; Score 456; DB 2; Length 249;
Best Local Similarity 45.6%; Pred. No. 3.4e-29;
Matches 99; Conservative 44; Mismatches 64; Indels 10; Gaps 5;
Qy 5 RVITLTVP-SDVNVSEIYQV-APQYVQALTLAKYFQGA-----DGSTLRPFDFKA 56
Db 25 RVITLRVEDPNEINLLSINEIDPNYILQAIMLANAFONALVPTSTDFGDALRFSMAKG 84
Qy 57 LOIANDI-PQAAVNTLNQTVQGVTVQVSMIDKIVDMKNVLSIVINDKKFWDQVTAI 115
Db 85 LEIANTITPMGAVSVYDQNTQTNNQVSMINKVLELVLTGLVGLVSGSVI-DQLTAIV 143
Qy 116 TMTFNLNSQSEAWIFYKEDAHKTSYYNVLFAIQDEETGGVMATPIAFDISVDIEK 175
Db 144 TMTFNLNTQNEAWIFWGKETANTQNTYNNVLFALQNAQTGGVMYCVPGFEIKVSARK 203
Qy 176 EKVLFTVTKIDTENYAVTVKAINVVQALQSSRDSKVD 212
Db 204 EQLVFTTQDSASYNVNIQSLKFAQLVSSSQYPIAD 240

RESULT 3
A24044
28k parasporal crystal protein precursor - Bacillus thuringiensis subsp. israelensis
N:Alternate names: delta-endotoxin
N:Contains: 24k parasporal crystal protein; 25k parasporal crystal protein
C:Species: Bacillus thuringiensis subsp. israelensis
C;Date: 29-Aug-1987 #sequence_revision 29-Aug-1987 #text_change 09-Jul-2004
C;Accession: A24044; A60123; A24505; S02651
R:Waaijck, C.; Dullenans, A.M.; van Workum, M.E.S.; Visser, B.
Nucleic Acids Res. 13, 8207-8217, 1985
A;Title: Molecular cloning and the nucleotide sequence of the Mr 28,000 crystal protein
A;Reference number: A24044; MUID:86067227; PMID:4070003
A;Accession: A24044
A;Molecule type: DNA
A;Residues: 1-249 <WAA>
A;Cross-references: UNIPROT:P05069
A;Note: the authors translated the codon GAA for residue 204 as Gln
R:Gill, S.S.; Singh, G.J.P.; Hornung, J.M.
Infect. Immun. 55, 1300-1308, 1987
A;Title: Cell membrane interaction of Bacillus thuringiensis subsp. israelensis cytolysin
A;Reference number: A60123; MUID:87193126; PMID:3570465
A;Accession: A60123
A;Molecule type: protein
A;Residues: 31-41 <GLI>
A;Note: this amino-terminal sequence was found in both 24K and 25K forms of the purified
R:Ward, E.S.; Ellar, D.J.
J. Mol. Biol. 191, 1-11, 1986
A;Title: Bacillus thuringiensis var. israelensis delta-endotoxin. Nucleotide sequence and
A;Reference number: A24505; MUID:87086764; PMID:3025452
A;Accession: A24505
A;Molecule type: DNA
A;Residues: 1-249 <WARI>
R:Ward, E.S.; Ellar, D.J.; Chilcott, C.N.
J. Mol. Biol. 202, 527-535, 1988
A;Title: Single amino acid changes in the Bacillus thuringiensis var. israelensis delta-

A;Reference number: S02651; MUID:89011977; PMID:2845100
A;Accession: S02651
A;Status: not compared with conceptual translation
A;Molecule type: DNA
A;Residues: 1-249 <WAR2>
C;Comment: This protein is one of several from the parasporal protein inclusion that set
C;Superfamily: 28k parasporal crystal protein
C;Keywords: delta-endotoxin
F:1-30/Domain: signal sequence #status predicted <SIG>
F:31-249/Product: 28k parasporal crystal protein #status experimental <WAT>

Query Match 39.1%; Score 456; DB 2; Length 249;
Best Local Similarity 45.6%; Pred. No. 3.4e-29;
Matches 99; Conservative 44; Mismatches 64; Indels 10; Gaps 5;
Qy 5 RVITLTVP-SDVNVSEIYQV-APQYVQALTLAKYFQGA-----DGSTLRPFDFKA 56
Db 25 RVITLRVEDPNEINLLSINEIDPNYILQAIMLANAFONALVPTSTDFGDALRFSMPKG 84
Qy 57 LOIANDI-PQAAVNTLNQTVQGVTVQVSMIDKIVDMKNVLSIVINDKKFWDQVTAI 115
Db 85 LEIANTITPMGAVSVYDQNTQTNNQVSMINKVLELVLTGLVGLVSGSVI-DQLTAIV 143
Qy 116 TMTFNLNSQSEAWIFYKEDAHKTSYYNVLFAIQDEETGGVMATPIAFDISVDIEK 175
Db 144 TMTFNLNTQNEAWIFWGKETANTQNTYNNVLFALQNAQTGGVMYCVPGFEIKVSARK 203
Qy 176 EKVLFTVTKIDTENYAVTVKAINVVQALQSSRDSKVD 212
Db 204 EQLVFTTQDSASYNVNIQSLKFAQLVSSSQYPIAD 240

RESULT 4
B64595
hypothetical protein HP0605 - Helicobacter pylori (strain 26695)
C;Species: Helicobacter pylori
C;Date: 09-Aug-1997 #sequence_revision 09-Aug-1997 #text_change 09-Jul-2004
C;Accession: B64595
R:Tomb, J.F.; White, O.; Kerlavage, A.R.; Clayton, R.A.; Sutton, G.G.; Fleischmann, R.D.;
Peterson, S.; Loftus, B.; Richardson, D.; Dodson, R.; Khalak, H.G.; Glodek, A.; McKenne-
son, J.D.; Kelley, J.M.; Cotton, M.D.; Weidman, J.M.; Fujii, C.; Bowman, C.; Watthey, L.
Nature 388, 539-547, 1997
A;Authors: Wallin, E.; Hayes, W.S.; Borodovsky, M.; Katpk, P.D.; Smith, H.O.; Fraser, C.
A;Title: The complete genome sequence of the gastric pathogen Helicobacter pylori.
A;Reference number: A64520; MUID:97394467; PMID:9252185
A;Accession: B64595
A;Status: preliminary; nucleic acid sequence not shown; translation not shown
A;Molecule type: DNA
A;Residues: 1-477 <TOM>
A;Cross-references: UNIPROT:O25326; GB:AE000574; GB:AE000511; NID:g2313721; PIDN:AAD0767

Query Match 8.8%; Score 103; DB 2; Length 477;
Best Local Similarity 20.5%; Pred. No. 1.3;
Matches 47; Conservative 54; Mismatches 90; Indels 38; Gaps 10;
Qy 2 PFN---RVITLTVP-----SSDVNVSEIYQVAPQYVQALTLAKYFQGA---DGSTLRPF 51
Db 199 YFNRLARMLAQKLEQIKTKIDKIVTKLYDKGLTTTIDDLQSLKA--QGNLSEYDILDQPF 256
Qy 52 DFEKALQIANDIPQAAVNTLNQTVQGVTVQVSMIDKIVDMKNVLSIVINDKKFWDQV 111
Db 257 ALEQNRLTLEVLTNLSVKNLKKTITIDAPNLQRRQD-LVSLREQISAIRYQNKQL---- 311
Qy 112 TAAITNTFTNLNSQSEAWIFYKEDAHKTSYYNVLFAIQDEETGGVMATPIAFDISV 171
Db 312 -----NYPKIDVDFS--WLFWIKQPAVATGRFGN--FYPGQONTAGTATLNIPTDGL 362
Qy 172 DIEKEKLVFTVTKIDTENYAVTVKAINVVQALQSSRDS 208
Db 363 SLQKQSIMLGQLANEKNLAYKKLQKDEQLYRKSLDIPARAKIESKAS 411

RESULT 5

F71918
hypothetical protein jhp0552 - Helicobacter pylori (strain J99)
C:Species: Helicobacter pylori
A:Variety: strain J99
C:Date: 12-Feb-1999 #sequence_revision 12-Feb-1999 #text_change 09-Jul-2004
C:Accession: F71918
R:Alm, R.A.; Ling, L.S.L.; Moir, D.T.; King, B.L.; Brown, E.D.; Doig, P.C.; Smith, D.R.;
Ives, C.; Gibson, R.; Merberg, D.; Malls, S.D.; Jiang, Q.; Taylor, D.E.; Vovis, G.F.;
Nature 397, 176-180, 1999
A:Title: Genomic sequence comparison of two unrelated isolates of the human gastric path
A:Reference number: A71800; MUID:99120557; PMID:9923682
A:Accession: F71918
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-477 <ARN>
A:Cross-references: UNIPROT:Q9ZLM7; GB:AE001487; GB:AE001439; NID:g4155086; PIDN:AA0612
A:Experimental source: strain J99
C:Genetics:
A:Gene: jhp0552

Query Match 8.7%; Score 101; DB 2; Length 477;
Best Local Similarity 20.1%; Pred. No. 1.9;
Matches 46; Conservative 55; Mismatches 90; Indels 38; Gaps 10;
Qy 2 PFN---RVITLTP-----SSDVVNYSEIYQVAPQVYNQALTLAKYFQGA1----DGLTLRF 51
Db 199 YFNILARMIALQKLEQIQTDIKRVTGLTIDDLQSLKA--QGNLSEYDILDMQF 256
Qy 52 DPEKALQIANDIPQAAVNTLNQTVQGVQVSVMDIKVIDIMKNVLSIVIDNKKFWDQV 111
Db 257 ALEQNRILTLEYUTNLSVKNLKTITDAPNLQRERQD-LVSRQISALRYQNKQI---- 311
Qy 112 TAAITNTFTNLNSQSEAWIFYKEDAHKTSYYNINLFAIQDEETGGVMATLPIAFDISV 171
Db 312 ----NYPKIDVPDS--WLFWIKPYPATGFGN--FYPGQNTAGVTATLNIFFDGL 362
Qy 172 DIEKKEVLFTVTKOTENVA-----VTVKAINVQVA-LQSRDS 208
Db 363 SIQKQSIMLQGLANEKNLAYKLEQKDEQRLYKSLIDIRAKIESKAS 411
RESULT 6
T30838
cytoplasmic dynein heavy chain - Paramesidium tetraurelia
C:Species: Paramesidium tetraurelia
C:Date: 22-Oct-1999 #sequence_revision 22-Oct-1999 #text_change 09-Jul-2004
C:Accession: T30838; PC4341
R:Kandl, K.A.; Forney, J.D.; Asai, D.J.
submitted to the EMBL Data Library, January 1995
A:Description: The dynein genes of Paramesidium: the differential expression of axonemal a
A:Reference number: Z20502
A:Accession: T30838
A:Status: preliminary; translated from GB/EMBL/DBDJ
A:Molecule type: DNA
A:Residues: 1-4540 <KAN>
A:Cross-references: UNIPROT:Q27171; EMBL:U20449; NID:g987228; PIDN:AAA75445
R:Asai, D.J.; Beckwith, S.M.; Kandl, K.A.; Keating, H.H.; Tjandra, H.; Forney, J.D.
J. Cell Sci. 107, 839-847, 1994
A:Title: The dynein genes of Paramesidium tetraurelia: Sequences adjacent to the catalytic
A:Reference number: PC4340; MUID:94334383; PMID:8056840
A:Accession: PC4341
A:Molecule type: mRNA
A:Residues: 1831-2029 <ASA>
C:Genetics:
A:Genetic code: SGC5
A:Introns: 57/3
C:Superfamily: dynein heavy chain, cytosolic

Query Match 8.5%; Score 99.5; DB 2; Length 4540;
Best Local Similarity 21.6%; Pred. No. 49;
Matches 58; Conservative 47; Mismatches 90; Indels 73; Gaps 12;
Qy 16 VVNYSEIYQVAPQ-----YVYNQALTLAKYFQGAIDGSTLRFDFEKAQIANDIPQAAVNT 71

Db 896 LVNQTVVHLEKLDQDIIVDPPEVYAKYFWFO-----EFHKMIGQCSLPR-LVANR 946
Qy 72 LNQTVOQGT-----VQVSVMDKI----- 90
Db 947 PDNTIQNTGPGTQRDLDSYTTINKINQLIKDAYSQIGQLLEDMEQVYVQVTLNYSQSLW 1006
Qy 91 -VDIMKNVLSIVIDNKKFWDQVTAATN---TFTNLNSQES-EMAFYFKEDAHKTSYYY 145
Db 1007 ELDI-KQVEQILQDDIEKQQQMLTDIKQGRATFDNSTTEEHGFAIIDIYRMVQVQKINHKY 1065
Qy 146 NILFAIQDEETGGVMATLPIAFDISVDIEKSKVLFVTIKDTENYATVVKAINVQVQALQSS 205
Db 1066 DAWHKELLNHNFGNKEGQRLVFNKNVTEKEKLLKINFDQLT--SDIIESIIFIQ-----E 1119
Qy 206 RDSKV-----VDAFKS-PRHLPKRHK 226
Db 1120 QDKKPPGWSADIESPKNGQKVLDRQRYQ 1147

RESULT 7

A1874
transcription repressor of class I heat-shock gene hrca - Bacillus subtilis
N:Alternate names: hypothetical protein 39
C:Species: Bacillus subtilis
C:Date: 03-May-1994 #sequence_revision 03-May-1994 #text_change 09-Jul-2004
C:Accession: A1874; G69642; S27503
R:Wetzstein, M.; Voelker, U.; Dedio, J.; Loebau, S.; Zuber, U.; Schiesswohl, M.; Herget,
J. Bacteriol. 174, 3300-3310, 1992
A:Title: Cloning, sequencing, and molecular analysis of the dnaK locus from Bacillus sub
A:Reference number: A1874; MUID:92250426; PMID:1339421
A:Accession: A1874
A:Molecule type: DNA
A:Residues: 1-343 <NET>
A:Cross-references: UNIPROT:P25499; EMBL:M84964; NID:g143056; PIDN:AAA22526.1; PID:g1431
R:Kunat, P.; Ogasawara, N.; Moszer, I.; Albertini, A.M.; Alloni, G.; Azevedo, V.; Berte
C.; Bron, S.; Brouillet, S.; Bruchli, C.V.; Caldwell, B.; Capuano, V.; Carter, N.M.; Ch
A.; Ehrlich, S.D.; Emmerison, P.T.; Entian, K.D.; Errington, J.; Fabre, C.; Ferrari, E.
Nature 390, 249-256, 1997
A:Authors: Foulger, D.; Fritz, C.; Fujita, M.; Fujita, Y.; Fuma, S.; Galizzi, A.; Galle
iech, J.; Harwood, C.R.; Henaut, A.; Hilbert, H.; Holsappel, S.; Hosono, S.; Hullo, M.F
Koetter, P.; Koningstein, G.; Krogh, S.; Kumano, M.; Kurita, K.; Lapidus, A.; Lardinois
A:Authors: Lauber, J.; Lazarevic, V.; Lee, S.M.; Levine, A.; Liu, H.; Masuda, S.; Maues
Y, M.; Ogawa, K.; Ogiwara, A.; Oudega, B.; Park, S.H.; Parro, V.; Pohl, T.M.; Portecell
Rieger, M.; Rivolta, C.; Rocha, E.; Roche, B.; Rose, M.; Sadate, Y.; Sato, T.; Scanlon
A:Authors: Schleicher, S.; Schroeter, R.; Scoffone, P.; Sekiguchi, J.; Sekowska, A.; Sero
akeuchi, M.; Tamakoshi, A.; Tanaka, T.; Terpestra, P.; Tognoni, A.; Tosato, V.; Uchiyama,
T.; Winters, P.; Wipat, A.; Yamamoto, H.; Yamane, K.; Yasumoto, K.; Yata, K.; Yoshida, I
A:Authors: Yoshikawa, H.F.; Zumstein, E.; Yoshikawa, H.; Danchin, A. Bacillus subtilis.
A:Title: The complete genome sequence of the Gram-positive bacterium Bacillus subtilis.
A:Reference number: A69580; MUID:98044033; PMID:9384377
A:Accession: G69642
A:Status: nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 1-343 <KAN>
A:Cross-references: GB:Z99117; GB:AL009126; NID:g2634966; PIDN:CAB14491.1; PID:g2634995
A:Experimental source: strain 168
C:Genetics:
A:Gene: hrca
C:Superfamily: conserved hypothetical protein MG205
C:Keywords: heat shock; stress-induced protein

Query Match 8.3%; Score 96.5; DB 2; Length 343;
Best Local Similarity 20.7%; Pred. No. 2.9;
Matches 47; Conservative 38; Mismatches 83; Indels 59; Gaps 8;
Qy 14 SDVNYSEI-----YQVAPQVYNQALTLAKYFQGAIDGSTLRF-----DF 53
Db 115 SDLTNTYSIVLGPLKSENLYKQIQIPIQPDMVAIVLTNTGHVENKTNFTFKMDLSDI 174
Qy 54 EKALQIANDIPQAAVNTLNQTVQGVQVSVMDIKVIDIMKNVLSIVIDNKKFWDQVTA 113
Db 175 EKLNVNILDRLSGVPMDELNER-----IFKEVVMYLRQHKYNYDILD 217

